us-09-880-457-1_copy_486_746.rni

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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                 NO.
                                                                                                                                                                                                                                                                                                            pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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December 8, 2002, 15:56;19; Search time 15.2491 Seconds (without alignments) 5249.015 Million cell updates/sec
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261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                              Listing first 45 summaries
                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                   Match
 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*/cgn2_6/ptodata/1/ina/5B_COMB.seq:*/cgn2_6/ptodata/1/ina/6A_COMB.seq:*/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*/
                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                    Length DB
    US-08-996-139-12
US-08-995-659-12
US-09-215-649A-12
US-09-577-780-12
US-09-577-780-12
US-08-996-139-10
US-08-996-139-10
US-08-995-659-10
US-08-995-659-10
US-08-984-26-6
US-09-052-521C-1
US-08-984-842-6
US-09-003-574-22
US-09-003-574-22
US-09-003-574-21
US-09-003-574-21
US-09-003-574-21
US-09-003-574-21
US-09-003-574-21
US-09-003-574-21
US-09-003-574-1
US-09-003-574-1
US-09-003-574-3
US-09-003-574-3
US-09-003-574-3
      US-09-003-574-30
                        US-09-003-574-32
                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                           Sequence 12, Appl
sequence 12, Appl
sequence 12, Appl
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sequence 3, Appli
sequence 10, Appl
sequence 10, Appl
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US-08-996-139-12
                                               Application US/08996139
                                                              US-09-003-570-30
US-08-463-262A-2
US-08-463-989-2
US-09-003-574-2
US-09-003-574-2
US-09-003-570-2
US-09-003-570-2
US-09-003-570-2
US-07-824-447-47
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-469-203A-7
US-08-926-522-12
US-09-003-570-21
US-09-003-570-21
US-08-463-262A-1
                                   ALIGNMENTS
                                                                                                   Sequence 2, Appli
Sequence 2, Appli
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appli
Sequence 47, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence
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Sequence 21, l
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47, Appl
12, Appl
21, Appl
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Sequence 12, Applicat
patent No. 6017729
GENERAL INFORMATION:
                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPHONE: (206)583-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/
EILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: USSN 0
APPLICATION NUMBER: 07 MARCH 1997
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                             APPLICATION NUMBER: USSN
FILING DATE: 23 DECEMBER
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  FILING DATE: 07 MARC.
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 5.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 51 Uni
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
              TOPOLOGY: 1: MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                               NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                                               STRANDEDNESS:
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51 University Street
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                                        linear
cDNA
NO
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                                                                                                                                                                                                                                                      UMBER: USSN 08/772,330
23 DECEMBER 1996
                                                       single
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ANTI-SENSE: NO ORIGINAL SOURCE:

ORGANISM:

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RESULT 2
US-08-995-659-12
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  PRIOR APPLICATION DATA:
USSN 08/772,330
                                              CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-996-139-12
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
CORRESPONDENCE, 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 181;
                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 22 DEG
                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation, Law Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
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CLONE: huRANKL (full length)
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LOCATION: 1..
                                                                                                                                                                                                                                                                                  98101
                                                                                                                                                                                                                                                                                                          WA
                                                                                                                                                                                                                                                                                           USA
23 DECEMBER 1996
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74.8%; Pred. No. 1.3e-34;
ative 0; Mismatches 53; Indels 8;
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RESULT 3
US-09-215-649A-12
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; LOCATION:
US-08-995-659-12
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COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                           713 TA 714
                                                                                                                                                                                                                                                                                                                                                                    653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 712
                                                                                                                                                                                                                                                                                                                                                                                 176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGGAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                       593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCCAAGATCTCCA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                       APPLICANT: Anderson, Dirk M.
Galibert, Laurent
MarasKovsky, Eugene
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Homo
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Perkins, Patricia Anne
RECISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 285;
                                                                                                      ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                                                           Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.48;
74.88;
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SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-215-649A-12
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: 1996
APPLICATION NUMBER: USSN 08/9813,509
APPLICATION NUMBER: USSN 08/972,330
APPLICATION NUMBER: USSN 08/972,3
                                                                                                   Sequence 12, Application US/09577780 patent No. 6419929 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word for Power Macintosh 6.0.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCCAAGATCTCCA 592
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TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                 593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                    713 TA 714
                                                                                                                                                                                                                                                                                                                                                                           236 TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/215,649A
FILLING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.48;
74.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 121.2; DB 4; Length 954; Pred. No. 1.3e-34;
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US-09-577-780-12
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APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
AREFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 2852-A
REFERENCE/DOCKET NUMBER: 2852-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 OPERATING SYSTEM: Apple Operating System 7.5.5 OPERATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                     533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCA 592
                                                                                       593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
                                                                                                                    122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                           176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                 64 GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
236 TA 237
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                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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STATE: WA
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                                                                                                                                                                                                                                                                                   181; Conservative
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FILING DATE: <Unknown>
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TELEFAX: (206)233-0644
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                        46.4%; Score 121.2; DB 4; Length 954; 74.8%; Pred. No. 1.3e-34;
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FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
PRIOR APPLICATION NUMBER: US/08/052,521C
PRIOR APPLICATION NUMBER: 08/80,855
PRIOR APPLICATION NUMBER: 08/80,855
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-04-16
PRIOR FILING DATE: 1997-04-16
SOFTWARE: PATENTION NUMBER: 08/842,842
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTION NOS: 40
SOFTWARE: PATENTION NOS: 40
SOFTWARE: PATENTION NOS: 40
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; LOCATION: (185)..(1135)
US-09-052-521C-3
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                 APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                             COUNTRY:
                                                                                                STATE:
                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                    897 TA 898
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                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                              837 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 896
                                                                                                                                                                                                                                                                                                                                                                                                                   176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ACATGACTTTCAGCAAGGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        717 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTCCA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
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                                                                98101
                                                                                                           Seattle
                                                                                             WA
                                                                                                           51 University Street
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    46.4%; Score 121.2; DB 4; Length 2271;
Similarity 74.8%; Pred. No. 2.1e-34;
81; Conservative 0; Mismatches 53; Indels 8;
                                                                             USA
                                                                                                                  Immunex Corporation, Law Department
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RESULT 7
US-08-995-659-10
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                                                      645 CT 646
                                                                             585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
                                                                                                 175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                 525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
                                                                                                                                                  121 AACATGAGTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                      465 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206)587-04:
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        405 GGCAAGCCTGAGGCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 464
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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HYPOTHETICAL: NC
                                                                                                                                                                                                        63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                          3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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PRIOR APPLICATION DATA:
USSN 60/064,671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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TOPOLOGY: Lir
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ETT.TNG DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                 36.6%; Score 95.6; DB 3; Length 1630; 68.2%; Pred. No. 4.2e-25; ative 0; Mismatches 69; Indels 8;
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/ Sequence 10, Application US/08995659
/ Patent No. 6242213

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent

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us-09-880-457-1_copy_486_746.rni

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US-08-995-659-10
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
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OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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FILING DATE: 07 MARCH 1997
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                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                    CLONE: RANKL
                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                405 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 464
            121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                465 GETTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                  LIBRARY:
525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
                                                            63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                        3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
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                                                                                                                                                             36.6%; Score 95.6; DB 4; Length 1630;
Similarity 68.2%; pred. No. 4.2e-25;
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                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                      conservative
                                                                                                                                                                                                                                                                                            Mus musculus
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22 DECEMBER 1997
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                                                                                                                                                            0; Mismatches
                                                                                                                                                                 69; Indels 8; Gaps
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RESULT 8
US-09-215-649A-10
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Patent NO. 6271349
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
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                                                            US-09-215-649A-10
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                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
          Query Match
Best Local Similarity 68.2%;
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
NAME: Perkins, UMBER: 34,693
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: <Unknown>
                                                                              NAME/KEY: CDS
IOCATION: 3.884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                             ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/996,139
ETLING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION DATE: 23 DECEMBER 1996
ETLING DATE: 23 DECEMBER 1996
                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....KESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 OPERATING SYSTEM: Apple Operating System 7.6.0.1 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
     165;
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                  CLONE: RANKL
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     Conservative
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              0; Mismatches
                          Score 95.6; DB 4; Length 1630; Pred. No. 4.2e-25;
                         Indels
                                8; Gaps
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RESULT 9
US-09-577-780-10
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INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION UNMBER: 08/913,509
APPLICATION UNMBER: USSN 08/813,509
APPLICATION UNMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: USSN 08/772,330
APPLICATION NUMBER: 31,693
ATTORNEY,AGENT INFORMATION:
REGISTRATION NUMBER: 34,693
TELECHOME: Q050587-0430
TELEPHONE: (205)587-0430
TELEPHONE: (205)587-0430
       HYPOTHETICAL: NO
ANTI SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GG--CTCATAAAACGAGTCTTTCTTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, Dirk M. Galibert, Laurent
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                                                                                                                                         LENGTH: 1630 base pairs
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TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
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US-08-989-362-1
                                                                                                                              CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 60,
APPLICATION UNMER: US 60,
ATTORNEY/ACENT INFORMATION:
NAME: Ching, Edwin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08989362
Patent No. 6242586
                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-09-577-780-10 DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                        NAME: Ching, Edwin P. REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gorman, Daniel M. APPLICANT: Mattson, Jeanine D. TITLE OF INVENTION: Mammalian (TITLE OF INVENTION: Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                     APPLICATION NUMBER: US/0
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAATACCATCAATATCCCATGA 62
nucleic acid
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                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                 901 California Avenue
                                                                                                                                                                                                                                                                                                                                     USA
                                                              (650)852-9196
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LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                                                            DNAX Research Institute
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                                                                                                                                            MBER: US 60/032,846
13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian Cell Surface Antigens; Related
                                                                                                                                                                                                              US/08/989,362
                                                                                                      34,090
                                                                                          DX0686
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                      US-08-842-842-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08842842 Patent No. 5843678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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Local Similarity 68.2%;
es 165; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCCATGA 62
                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1840 Dehavis
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                      NAME/KEY:
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                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                TOPOLOGY:
                                                                                                               STRANDEDNESS:
                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                         91230-1789
                                                                                                                             nucleic acid
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1840 Dehavilland Drive
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SYSTEM: PC-DOS/MS-DOS
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36.6%; Score 95.6;
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    DB 2;
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    Length 2295;
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Query Match

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; LOCATION: (158)..(1105)
US-09-052-521C-1
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boyle, William J. TITLE OF INVENTION: Osteopro
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2295
TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 08/1
PRIOR APPLICATION NUMBER: 08/1
PRIOR TITNG DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 746 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          686 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 745
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                                                                                                                                                                                                                                                                           626 GGCAAGCCTGAGGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 685
                                                                                                                                                                                                      686 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 745
                                                                                                                                                                    121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                  806 GCCAACATTIGCTTICGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 865
                                                                                                  175 GCCGACATTTGCTCTCGACATCGCCTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                     746 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 805
866 CT 867
                                 235 CT 236
                                                                                                                                                                                                                            63 GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
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                                                                                                                                                                                                                                                                                                           3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
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                                                                                                                                                                                                                                                                                                                                                                      Score 95.6; DB 4; Length 2295; pred. No. 5.1e-25;
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Patent No. 6281345
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia Ann
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: NOVEL PARASITE ASTACIN
TITLE OF INVENTION: "AFALLOENDOPEPTIDASE GE
                                                                                                                                                                                                                                                                              US-09-003-570-22
                                                                                                                                                                                                                                                                                            RESULT 14
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
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                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LENGTH: 271 base pairs
                                                                       ADDRESSEE: SHERIDAN NOOS .... STITE 3500
                                                   COUNTRY:
                                                                    STATE:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: SHERIDAN ROSS P.C.
STREET: 1700 LINCOLN ST., SUITE 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: MOVEL PARASITE ASTACIN
TITLE OF INVENTION: METALLOENDOPEPTIDASE PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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STATE:
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CITY: DENVER
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(303) TD NO: 22:
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US-09-003-574-20
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Patent No. 6265198
GENERAL INFORMATION:
                                                                                             TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                           REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
MOLECULE TYPE:
                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
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MEDIUM TYPE: Floppy
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SHERIDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: NOVEL PARASITE ASTACIN
TITLE OF INVENTION: METALLOENDOPEPTIDASE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tripp, Cynthia Ann
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B
                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                              LENGTH:
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                         689 base pairs
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1700 LINCOLN ST., SUITE 3500
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Perfect score:
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Maximum DB seq length: 2000000000
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1 aaaagaggataattcaagaa.....taataaaaggaggaaaatgc 1161
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/6E_COMB.seq:*
/cgn2_6/ptodata/1/ina/pc=US_COMB.seq:*
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       US-08-996-139-12
US-08-995-659-12
US-09-215-649A-12
US-09-577-780-12
US-09-577-780-13
US-08-995-659-10
US-08-995-659-10
US-08-995-659-10
US-08-98-362-1
US-08-98-362-1
US-09-215-649A-10
US-08-232-636-1
US-09-246-63-1
US-09-252-521C-1
US-09-258-102-1
US-09-568-102-1
US-09-568-102-1
US-09-568-486-1
          US-08-952-736A-1
US-08-952-736A-2
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                                                                                                                                             Sequence 12, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 12,
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Patent No. 6017729
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE Immunex Corporation, Law Department
                                                                                       TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    FILING DATE: 07 MARC PRIOR APPLICATION DATA:
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                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                  HYPOTHETICAL:
                                              MOLECULE TYPE:
                                                                                                                                                                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
                                                                                                                                                                                                                                                   APPLICATION NUMBER: USSN OF FILING DATE: 07 MARCH 1997
                                                                                                                                           TELEPHONE:
                                                           TOPOLOGY:
                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 University Street
                                                                                  nucleic acid
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US-08-671-320-10

US-08-671-320-10

US-09-262-749-1

US-09-262-749-1

US-09-022-669-1

US-09-033-567-1

US-09-146-053-5

US-09-146-053-5

US-09-062-451-245

US-09-598-326-245

US-09-598-326-245

US-09-598-379-496-1

US-09-244-796-32

US-09-244-796-32

US-09-07-005-3
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US-08-599-252-103
PCT-US96-06352-103
PCT-US96-06583-103
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sequence 10, Appl
sequence 18, Appl
sequence 1, Appli
sequence 1, Appli
sequence 1, Appli
sequence 1, Appli
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sequence 103, App
sequence 103, App
sequence 103, App
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Sequence 245, App
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US-08-995-659-12
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07 MARCH
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 14 OCTOR
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M,
APPLICANT: Galibert, Laurent
TITLE OF INVENTION: Ligand for Receptor Activator of NF-KappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                    STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 193;
                                                                                                        CLASSIFICATION:
                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 22 DEC
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                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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                                                                                                              UMBER: USSN 60/064,671
.14 OCTOBER 1997
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                                                                    USSN 08/813,509
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Sequence 12, Application US/09215649A
PATENT NO. 6271349
PATENTION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
NUMBER OF SEQUENCES: 19
TITLE OF INVENTION: Receptor Activator of NF-kappaB
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US-09-215-649A-12
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; LOCATION:
US-08-995-659-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
COMPUTER: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                     697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
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SEQUENCE CHARACTERISTICS.
LENGTH: 954 base pairs
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HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 72.6%;
tes 193; Conservation
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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REGISTRATION NUMBER: 34,693
                                                                                                  CITY: Seattle
STATE: WA
                                                                                     COUNTRY: USA
                                                                                                             ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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US-09-215-649A-12
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                                                                                     Sequence 12, Application US/09577780 Patent No. 6419929
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCCAGCCTTCAACTCATCTTGTTA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                       629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
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                                                                                                                                                                                                                                                              689 ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                         697 GCCTAACTCTGCAGGACCTTCAGCTA 722
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-KappaB
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FILING DATE: CINKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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TYPE: nucleic acid
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LOCATION: 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: huRANKL (full length)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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72.6%;
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 Mismatches

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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/995,659
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34.693
                                                                                                                                                                                                                                                                                                    449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                            465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                             629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                   640 ---AAGGCATITATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                              569 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTAGCAATGGAAAACTAATAGTTAATC 628
                                                                                                                                                                       583 ACCAAGATIGGGCAAACGTCICCAACATGACTTICAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                           525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Power Macintosh operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                              10.9%;
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689 ACCTAGCTACAGAGTATCTTCAACTA 714

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US-08-996-139-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 08/880,855 PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/6 PRIOR FILING DATE: 1997-04-16
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SOFTWARE: Patentin Ver.
               COUNTRY: USA
ZIP: 98101
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME/KEY: CDS
LOCATION: (185)..(1135)
                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                                                                                                           TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2271
                                                                                                                                                                                                                                                                                                                                                                                                                  873 ACCTAGCTACAGAGTATCTTCAACTA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    813 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640 ---AAGGCATTTACTACCGGAATGCCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                693 TTAATGCCACCGACATCCCATCTGGTTCCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           753 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
COMPUTER: Apple Power Macintosh
                                                                                                    STATE:
                                                                                                                                      STREET:
                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 10.9%;
Local Similarity 72.6%;
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                                                                                                                  Seattle
                                                                                                WA
                                                                                                                                  E: Immunex Corporation, Law Department
51 University Street
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RESULT 7
US-08-995-659-10
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US-08-996-139-10
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus I
                                                                                                                                   574 ATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAG 633
                                                                        634 ACTATCTTCAGCT 646
                                                                                                        709 AGGACCTTCAGCT 721
                                                                                                                                                                                                         514 CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCT 573
                                                                                                                                                                                                                              595 CAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTT 648
                                                                                                                                                                                                                                                                              454 GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG 513
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LENGTH: 1630 base pairs
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FILING DATE: 23 DECEMBER
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    537 ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTCTTGGAAAACATGACCAAGATTGGG 594
                                                                                                                                                                                                                                                                                                                                                    394 TGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACCACCATCAACCATCAATGCTGCCA 453
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APPLICATION NUMBER: USSN 0/
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
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                                                                                                                                                      ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
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Sequence 10, Application Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderso

Application US/08995659

APPLICANT:

Anderson, Galibert,

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                                                                                                                                                                                                       Matches 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: PERKINS, PATRICIA Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2852 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IFILING DATE: 07 MARCI CLASSIFICATION:
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
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STRANDEDNESS: SING
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                                                                                       537 ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGG 594
                                                                                                                                                                 477 TTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCA 536
                                                                                                                                   394 TGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 14 OCT CLASSIFICATION:
                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: USSN 08/7
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 22 DE
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                                                                                                                                                                                                                                                                                                                                                            LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                       Local Similarity
                 CAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTT 648
CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCT 573
                                                                GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                          RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Immunex Corporation, Law Department 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: (206)587-0430
(206)233-0644
POR SEQ ID NO: 10:
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER: USSN 60/064,671
14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 DECEMBER 1997
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                                                                                                                                                                                                                  8.4%;
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                                                                                                                                                                                                                   Score 97;
Pred. No.
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                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                DB 4;
. 8e-22;
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                                                                                                                                                                                                                                   Length 1630;
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                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-215-649A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09215649A Patent No. 6271349
GENERAL INFORMATION:
      Matches 170;
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/996,139

FILING DATE: «Unknown»

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                               FEATURE
                                                                                                                                                                                                                      ORGANISM: Mus musculus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maraskovsky, Bugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ACTATCTTCAGCT 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                                                                     NAME/KEY: CDS
LOCATION: 3..884
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                    LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1630 base pairs
                                                                                                                                                                                 ONE: RANKL
      Conservative
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                      8.4%;
67.2%;
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    0;
                    Score 97; DB 4; Length 1630; Pred. No. 8e-22;
    Mismatches
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PATENT NO. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                       TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.
SOFTWARE: Microsoft Word for Power Macintos
CURRENT APPLICATION DATA:
                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGIGFRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: «Unknown»
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/813,509
APPLICATION NUMBER: USSN 08/813,509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
IMMEDIATE SOURCE:
                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown>
                              ORGANISM: Mus musculus
                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation, Law Department
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Maraskovsky, Eugene
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US-08-989-362-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
                                                                GENERAL INFORMATION:
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pair
                                                                                                                                                                                   CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/032,846
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GORMAN, D
APPLICANT: Mattson,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 California Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jeanine D.
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Pred. No.
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FEATURE: MOLECULE TYPE:

NAME/KEY:

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TOPOLOGY: STRANDEDNESS:

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US-08-842-842-6
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Best Local Similarity 67.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
Query Match
                                                                                                                                                                                                  NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BOYLE, WILLIAM J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 TIGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCA 536
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                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                         MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: LOTE CITY: Thousand Oaks
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                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                     NAME/KEY:
                                                                                                                              TOPOLOGY:
                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                  LENGTH:
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                                                                                                                                                               nucleic acid
                                                                                                                                                                                    2295 base pairs
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125..1072
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 Mismatches

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                                                                                                                                                                                                                                            A-451
     Score 97;
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US-09-052-521C-1
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; LOCATION: (158)..(1105)
US-09-052-521C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPRO
FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/1 PRIOR FILING DATE: 1997-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mouse FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                   735 CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCT 794
                                                                                                                                                                                                            595 CAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTT 648
                                                                                                                                                                                                                                                      675 GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG 734
                                                                                795 ATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAG 854
                                                                                                       649 ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
855 ACTATCTTCAGCT 867
                                          709 AGGACCTTCAGCT 721
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67.2%;
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0; Mismatches 75; Indels
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pred. No. 1e-21; 
0; Mismatches 75; Indels
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US-08-232-463-14/c
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GENERAL INFORMATION:
GENERAL TOANT: DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                             356 CAAGGCACCAGGCATTTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAA 415
                                                                                          296 GGGGAGAGAAGTGGAGAGAGGACCTGGAGGGCCCAGTAGAAGGTATGCACACAAGTATCTA 355
                                                                                                                                                                                                                    176 CTTCAGGAACACCCTGCTTGAGAGGCCTGTGAGAGGTGGGGAATCAATACCTGACCTCGC 235
                                                                                                                                                                                                                                                                                 116 GGGATAAGGACGTGGTTGCGAGGACATGGAGGGAAAGTTCTACAGAGGAGGCACAGTGGG 175
                                                                                                                                                         236 TCTCCTTCCATCTCTCCCCAACCCACAGGGGTTGGTGTGGGGCCCCACAGGCGAGCCTCCC 295
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
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LOCATION: (1)...(289)
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ORGANISM: Artificial Sequence
FEATURE:
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4.6%; Pred. No. 0.021;
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GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.

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APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/04,491
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-07
SEARLIER FILING DATE: 1998-01-14
NUMBER OF SEO ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
FEATURE:
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  US-08-989-362-1
US-08-842-842-6
US-09-052-521C-1
US-07-968-971A-5
US-07-824-247-47
US-08-142-473A-7
US-08-464-233B-7
US-08-469-203A-7
US-08-469-203A-7
US-08-470-204A-47
US-08-966-522-12
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US-08-996-139-12
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                                                                                            TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Wood CURRENT APPLICATION DATA:
                                                                                                                                                NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOXET NUMBER: 2851 TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                    FILING DATE: 23 DECEMBER ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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HYPOTHETICAL:
                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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CLASSIFICATION:
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                                                   STRANDEDNESS:
                                                                    TYPE:
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                                                                                      954 base pairs
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                                    linear
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                                                                                                                                                                                                                                                                                                       NUMBER: USSN 08/813,509
07 MARCH 1997
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22 DECEMBER 1997
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23 DECEMBER 1996
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Patent No. 6242213
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                           ATTORNEY/AGENT INFORMATION: NAME: Perkins, patricia
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
APPLICANT: Anderson, Dirk M.
APPLICANT: Gallbert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                   APPLICATION NUMBER: FILING DATE: 23 DE
                                                     CLASSIFICATION:
                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                 APPLICATION NUMBER: USSN 60/064,671 FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                               CLASSIFICATION:
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SOFTWARE: MICTOSOft Word for Power Macintosh 6
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ORGANISM: Hom
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IMMEDIATE SOURCE:
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LOCATION:
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                                                                   23 DECEMBER 1996
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                                                                              USSN 08/772,330
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US-09-215-649A-12
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 GCTA 180
 COMPUTER: Apple Form againtosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
RAPPLICATION DATA:
APPLICATION WIMBER: US/09/215,649A
FILLING DATE: 17-Dec-198
CLASSIFICATION: <UNKnown>
APPLICATION UNMBER: 08/996,139
PRIOR APPLICATION NUMBER: 08/996,139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
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LENGTH: 954 base pairs
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                                                                                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
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                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, Dirk M.
Galibert, Laurent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                     STATE: WA
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Maraskovsky, Eugene
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SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-215-649A-12
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US-09-577-780-12
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                                                                                                                                                                                                                                                       Sequence 12, Application US/09577780 Patent No. 6419929
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                           Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137;
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M.
Galibert, Laurent
                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07 MARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 47.3%;
Similarity 74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: <Unknown>
                                                                                                                                 ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                 CITY: Seattle
                                                                                     COUNTRY: USA
                                                                                                   STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96.4; DB 4; Length 954; pred. No. 3.7e-26;
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SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-577-780-12
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                                                                                                                                                                                           RESULT 5
US-09-052-521C-3
                                                                                                                                         ; GENERAL INFORMATION:
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                                                                                                                                                         Sequence 3, Application US/09052521C Patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 12:
FILE REFERENCE: A-451BrV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
                                                                                                 APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
                                                                                                                                                                                                                                                                                                                                                                       117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                      711 ACTA 714
                                                                                                                                                                                                                                                                                                      177 GCTA 180
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/995,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
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TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: huRANKL (full length)
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LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                           A-451Brv
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74.58;
                                                                                                           Osteoprotegerin Binding Proteins and Receptors
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PRIOR FILING DATE:

1997-04-16

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US-08-996-139-10
APPLICATION UNMER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION UNMER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PALTICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TÉLECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
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LENGTH: 2271

TYPE: DNA
ORGANIAM: Human
FEATURE:
PAME/KEY: CDS
LOCATION: (185)...(1135)
                                                                                                                                                                      APPLICATION NUMBER: USSN 60/1
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 MEDIOM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
APPLICATION UNIVERS.
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/996 FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          895 ACTA 898
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       835 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 47.3%; Score 96.4; DB 4; Length 2271; Local Similarity 74.5%; Pred. No. 5.9e-26;
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o. 6017729
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                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunex Corporation, Law Department
                                                                                                                                                                                                           USSN 60/064,671
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US-08-995-659-10
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Patent No. 6242213
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                              PRIOR APPLICATION DATA;
APPLICATION NUMBER: USSN 0
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: USSN 60/064,671
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TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                     CLASSIFICATION
                                                                                                   APPLICATION NUMBER: FILING DATE: 14 OC'
                                                                                        CLASSIFICATION:
                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 22 DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589 ACATTTGGTTTGGGCATCATGAAACATCGGGAAGCGTAGCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ACATTIGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
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                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGGCCAAGATCTCTAACA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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LOCATION:
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CLONE: RANKL
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                                                                                                                                                                  22 DECEMBER 1997
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                                                                                                     14 OCTOBER 1997
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                                             USSN 08/813,509
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                                                                                                                                                                                US/08/995,659
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; LOCATION:
US-08-995-659-10
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                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09215649A Patent No. 6271349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 23 DECCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 TGACTITCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENSE:
                                                                                                                                                                                                                                                                               Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1630 base pairs
                                                                               COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                    STATE: WA
                                                                                                                                                                                                                    CITY: Seattle
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23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                       Galibert, Laurent
                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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US-09-215-649A-10
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US-09-577-780-10
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, Patent NO. 6419929
, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 ACATTTCCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCAFTTATTACCGGAATGCCG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
                                                                                                                                                                                                                                                       Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                          STATE: WA
                                                                                                                                       COUNTRY:
                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09577780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.6%; Score 80.8; DB 4; Length 1630; 70.2%; Pred. No. 3.2e-20;
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                              Macintosh 6.0.1
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APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000

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US-08-989-362-1
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                                                                                                                                                                                                                                                                    sequence 1, Application US/08989362
Patent No. 6242586
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                     APPLICANT: Gorman, Daniel M. APPLICANT: Mattson, Jeanine D. TITLE OF INVENTION: Mammalian (TITLE OF INVENTION: Reagents
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                    589 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
                                       COUNTRY: USA
ZIP: 94304-1104
                                                                      CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                     122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                       529 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACA 528
                                                                                                         STREET:
                                                                                                    ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: RANKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Floppy disk
                                                                                                                                                                                Mammalian Cell Surface Antigens; Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.6%;
70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <Unknown>
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US-08-842-842-6
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                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-989-362-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
REFERENCE/DOCKET NUMBER:
                                                                           FILING DATE:
                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 91230-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUFFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGGAATGCCG 121
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 39.6%; Score 80.8; DB 4; Length 2191; Cocal Similarity 70.2%; Pred. No. 3.7e-20; es 125; Conservative 0; Mismatches 47; Indels 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                 Thousand Oaks
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                               E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2191 base pairs
                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
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A-451
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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US-08-842-842-6
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                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS; LOCATION: (158)..(1105) US-09-052-521C-1
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                                                                                                                       밁
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RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 1, Application US/09052521C Patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                          Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/1
PRIOR EILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/1
PRIOR EILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mouse
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       690 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCCTGGGCCAAGATCTCTAACA 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    750 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 39.6%;
Local Similarity 70.2%;
es 125; Conservative
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                                                   810 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 867
                                                                                  122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                      750 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 809
                                                                                                                                                                                        690 CCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCCTGGGCCAAGATCTCTAACA 749
                                                                                                                                                       68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                                                             Match 39.6%;
Local Similarity 70.2%;
                                                                                                                                                                                                                       8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80.8; DB 2; Length 2295;
Pred. No. 3.8e-20;
                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                               Score 80.8; DB 4; Length 2295; pred. No. 3.8e-20;
                                                                                                                                                                                                                                                                       47; Indels
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US-07-968-971A-5

; Sequence 47, Application US/07824247

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US-07-824-247-47

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Sequence 5, Application US/07968971A Patent No. 5455167
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                                                                                                                                                                   Query Match
                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                            TELEFAX: (916) 753-15
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Toni A. Voelker
APPLICANT: Huw Maelor Davies
TITLE OF INVENTION: Medium-Chain Thioesterases
TITLE OF INVENTION: In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh (
OPERATING SYSTEM: Macintosh (
SOSTWARE: Microsoft Word 4.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: 07/704,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8:
FILING DATE: 22-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
1301 AATATCAGAAAAATAACTCAATGAGTCAAGGTTAT 1335
                                                                   1241 CAGAATCATGGCCTGTGGTTTTAGATATATATCCAAAATTGTCCTATAGTCAAGAAACTT 1300
                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Davis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/
FILING DATE: 7-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/782,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                  10 CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATG 69
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME:
                                 70 ACTITCAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                        54; Conservative
                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1920 Fifth Street
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                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                     (916) 753-6313
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                                                                                                                                                                                                                               PCR - generated DNA from mRNA
                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                                      753-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macintosh 6.0.7
                                                                                                                                                          14.4%; Score 29.4; DB 1; Length 1461; 56.8%; Pred. No. 0.4;
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                                                                                                                                             Mismatches
                                                                                                                                                   41; Indels
                                                                                                                                                     0;
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Patent No. 5512482

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US-07-824-247-47
                                                                                                                          Matches
                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
1301 AATATCAGAAAAATAACTCAATGAGTCAAGGTTAT 1335
                                                 1241 CAGAATCATGGCCTGTGGTTTTAGATATATCCAAAATTGTCCTATAGTCAAGAAACTT 1300
                                                                                                                                                                                     MOLECULE TYPE: PCR product from mRNA template
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 916-753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-APR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/6
FILING DATE: 27-FEB-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-APR-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/662,007
                          70 ACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                                  10 CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/71
FILING DATE: 21-MAY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                      Local
                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Voelker, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/620,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 25-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/773,096 FILING DATE: 7-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/7 FILING DATE: 24-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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STATE: Cali
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                                                                                                                          54;
                                                                                                                                   Similarity
                                                                                                                                                                                                                                     NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                              Elizabeth Lassen
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                                                                                                                       Conservative
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                                                                                                                                   14.4%;
56.8%;
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                                                                                                                     0,
                                                                                                                             Score 29.4; DB 1; Length 1461; Pred. No. 0.4;
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                                                                                                                 Mismatches 41;
                                                                                                               Indels
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                                                                                                                                        Matches
                                                                                                                                                         Query Match
Best Local :
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US-08-142-473A-7
                                                                                                                                                                                                                                                                                                             TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08142473A
Patent No. 5639790
GENERAL INFORMATION:
1301 AATATCAGAAAAATAACTCAATGAGTCAAGGTTAT 1335
                                                        1241 CAGAATCATGGCCTGTGGTTTTAGATATATATCCAAAATTGTCCTATAGTCAAGAAACTT 1300
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                            MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/773,096
FILING DATE: 7-0CT-1991
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APPLICATION NUMBER:
FILING DATE: 24-OCT-
                              70 ACTITCAGCAACGGAAAACTAAGAGTCAAAGGCAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                     10 CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/824,247
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OPERATING SYSTEM: Macintosh 7
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                          TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Donna E. Scherer
REGISTRATION NUMBER: 34
NAME: Carl J. Schwedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Plant Thioesterases
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/8:
FILING DATE: 22-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 21-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Davis
STATE: California
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1920 Fifth Street
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21-MAY-1992
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Search completed: December 8, 2002, 17:28:32 Job time : 17.9188 secs

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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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			Sequence 1, Appli	sequence John Fr	Eccuence 334. App	Sequence y, APPLL	Cucured 1	segmence 5, Appli	Sequence Soos, AP	CHACE CONT.	secmence 8. Appli	Sequence 4, APP11	ocyucaco	compance 11, Appl	Sequence II, APPI	Cquesto 11	Secmence 14, Appl	Sequence 2, APPLL		segmence 13, Appl	Sequence /, Appri	Caccaca 7 Appli	•	Sequence 15, Appl			"	Sequence 4, Appli	Describeron

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Sequence 422, App	(U	16		Sequence 6, Appli	9	Sequence 12, Appl	Sequence 7, Appli	9	ú			4	Sequence 4, Appli	Sequence 4, Appli	4	sequence 39850, A	,,,	Sequence 2, Appli	느	N	16	Sequence 10, Appl	sequence 42049,	

ALIGNMENTS

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US-09-880-457-4
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US-09-880-457-4
; Sequence 5, Application US/09880457; Patent No. US20020106728A1; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: 90-96-12
CURRENT APPLICATION UNMBER: US-60/212,901
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                          RESULT 2
US-09-880-457-5
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US-09-779-050A-15

; Sequence 15, Application US/09779050A

; Patent No. US20020160416A1
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: SEQ ID NO 5
: LENGTH: 94
: TYPE: PRT
: ORGANISM: HOMO Sapiens
US-09-880-457-5
                                                                                           GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/779,050A
                      APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
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APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09880457 Patent No. US20020106728A1
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PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
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TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
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    Mismatches

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US-09-877-650-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application UPatent No. US20020169117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-779-050A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 15
LENGTH: 160
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206)587-04.
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILLING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILLING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NEWLY SAME TO THE TONEY AGENT TONEY 
                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Un-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                               LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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   47.7%; Score 178; DB 9; Length 317; 60.0%; Pred. No. 2.7e-15; ative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206)587-0430
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Gaps
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 7
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Patent No. US20020012968A1
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
                                                                         APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Receptor Activator of NF-kappaB
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Pred. No. 2.7e-15;
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US-10-017-910-2
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                               Query Match
Best Local Similarity
                Matches
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-017-910-2
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                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 47.7%;
Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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TELEFAX: (206)233-0644
                                                                                                                                                                                   LENGTH: 245 amino acids
                                                                                                                                                                                                                                            TELEX: 133521
                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 317 amino acids
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi, Yongwon
Wong, Brian
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46.6%; Score 174; DB 9;
58.3%; Pred. No. 6.4e-15;
tive 5; Mismatches 18
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                                                                                                   2:
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                                   Length 245;
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  Indels
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RESULT 10
US-09-877-650-11
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US-09-779-050A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Mus musculus US-09-779-050A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
IFFERTMENT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 56.7 nes 34; Conservative
                                                                                                                                                                                                                      FILING DATE: 08-Jun-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101
COMPUTER READABLE FORM:
                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHKVSLSSWYHDRGWGKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL
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                                                                                                  APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                          REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/877,650
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                              NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
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56.7%;
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Pred. No. 6.8e-15;
6; Mismatches 18
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US-09-871-856-11
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                        Matches
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-09-871-856-11
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                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/871,856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson, Dirk M. Galibert, Laurent
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34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                         LENGTH: 294 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                         TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word for Power
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WA
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  Conservative
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56.78;
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                    46.1%;
56.7%;
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  6,
                    Score 172; DB 10;
Pred. No. 1.4e-14;
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Pred. No. 1.4e-14;
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  Mismatches
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                                      DB 10;
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                                      Length 294;
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Indels
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Gaps
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Patent No. US20020159970A1
GENERAL INFORMATION:
APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-017-910-4
                                                                                                                                                                  US-09-911-777-8
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                                                                                                 Sequence 8, Application US/09911777
Patent No. US20020037852A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                            APPLICANT: BIOGEN, INC. APPLICANT: APOTECH S. I
                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
APPLICANT:
                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 SHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
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                                                                                                                                                                                                                                                                                                                                                        Match 46.1%;
Local Similarity 56.7%;
                                                                                                                                                                                                                                                                                          3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARRE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION UNMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 316 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                      APOTECH S.A.
BROWNING, Jeffrey
AMBROSE, Christine
  MACKAY, Fabienne
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                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Score 172; DB 9; Length 316; Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                               18; Indels
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; ORGANISM: Homo Sapien US-09-911-777-8
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                                                                  ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5085
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use TITLE OF INVENTION: in the Modulation of B-Cell Response FILE REFERENCE: A070 US CURRENT APPLICATION NUMBER: US/09/911,777 CURRENT FILING DATE: 2001-07-24
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PRIOR ETLING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR ETLING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: PCT/US00/01788
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                                                                                                                              NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5085
LENGTH: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                     Query Match
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 50/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQL 60
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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SCHNEIDER, Pascal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.2%; Score 112.5; DB 10; Length 109; 41.4%; Pred. No. 1.6e-07;
       17.0%; Score 63.5; Di 28.8%; Pred. No. 3.5;
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                                 DB 10;
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                                   Length 813;
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Matches

19;

Conservative

11; Mismatches

23;

Indels

13;

Gaps

Best

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GENERAL INFORMATION:

APPLICANT: Dilley, David R

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Wang, Zhenyong

APPLICANT: Warner, Toni M

TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
FILE REFERENCE: MSU41-453

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US/09/924,841

PRIOR FILING DATE: 1999-10-06

PRIOR FILING DATE: 1999-10-06

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 329

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
NAME/KEY: MUTAGEN
COTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-5
Search completed: December 8, 2002, 19:36:16 Job time: 11.0903 secs
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US-09-924-841-5
Sequence 5, Application US/09924841
Patent No. US20020127633A1
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                                                                                                                                                                                                                                                     Query Match 16.0%; Score 59.5; DB 10; Length 329; Best Local Similarity 25.7%; Pred. No. 3.7; Matches 18; Conservative 10; Mismatches 33; Indels 9;
                                                                                      120 GTPMHEVNLW 129
                                                                                                                                52 GLTLQDLQLW 61
                                                                                                                                                              60 NEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPMIAA 119
                                                                                                                                                                                                      1 HEAHKTSLSSWKHD------QDWANVSNMTFS--NGKLRVKGIYYRNADICSRHRVTSA 51
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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455
1 MAILTLSLQLILLLIPSISH.....TSAGLTLQDLQLWCNLRIIH 87
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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// Ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
// Ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
// Ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 3 3 4 4 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
455 440 440 440 180.5 180.5 176.5 176.6 17	Score
100.0 96.7 95.4 95.4 39.7 39.7 39.7 39.7 38.8 38.7 38.7 38.7 13.8 13.5 13.5	Query Match Length
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Sequence 4, Appli Sequence 5, Appli Sequence 15, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 2, Appli Sequence 14, Appli Sequence 11, Appli Sequence 11, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	. []

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US-09-855-544A-13	US-09-815-242-12814	US-09-815-242-12447	US-09-443-440-4	US-09-280-136-3	US-09-921-66/-4	US-09-764-868-1192	US-09-779-050A-19	US-09-801-368-326	US-09-824-588-2	US-09-801-366-200	S-09-764-808-966	US-09-864-701-45647	05-10-115 / 13 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	US-U9-042-74JA-1	CO-04-904-400-40	170-00-034-465-16	US 10 000 000 1	US-05 525 531-2	WS-09-001-301-866	05 05 050 555 555	ms-09-925-302-760	US-09-001-000 III	368-	ne-09-815-242-4986
Sequence 13, Appl	Sequence 12014, Ap		sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 4, Appli	sequence 1192, Ap	sequence 19, Appl	seguence 326. App	sequence 2, Appli	Sequence 266, App	Sequence 883, App		-	sequence 2, Appli	느	Sequence 10, Appl	Sequence 2, Appli	Sequence 866, App	Sequence 334, App	Sequence 760, App	Sequence 10, Appl	Sequence 176, App	Sequence 4986, Ap

ALIGNMENTS

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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
TITLE OF INVENTION: FOR THE TREATMENT OF BODY WEIGHT DISORDERS THE TREATMENT OF THE TREATMENT
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US-09-880-457-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO 4
; LENGTH: 87
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GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
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; Sequence 6, Application US/09880457

; Patent No. US20020106728A1
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                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 455; DB 10; Length 87; Best Local Similarity 100.0%; Pred. No. 1.3e-49; Matches 87; Conservative 0; Mismatches 0; Indels C
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CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/212,901 PRIOR FILING DATE: 2000-06-20
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US-09-779-050A-15
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CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
LENGTH: 94
TYPE: PRT
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                                                                                                                                                                                    RESULT 4
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                                                                                                 Sequence 15, Application US/09779050A Patent No. US20020160416A1 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/779,050A
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                            TITLE OF INVENTION: RECEPTOR FROM THE FAMILY FILE REFERENCE: A-570B
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                                                                   APPLICANT: BOYLE, WILLIAM APPLICANT: HSU, HAILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-880-457-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use FILE REFERENCE: P2871R1

TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
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SEQ ID NO 6
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TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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nes 83; Conservative
                                                                                                                                                                                                                                                                                     1 MAILMESLQLILLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD 60
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                                                                                                                                                                                                                                                                                                                                                            95.4%; Score 434; DB 10; Length 94; 96.5%; Pred. No. 5.6e-47; rative 1; Mismatches 2; Indels
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Pred. No. 1e-47;
""" and tches 1; Indels
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US-09-877-650-13
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                                                                     TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
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TYPE: PRT
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    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION CURRENT OB-JUN-2001
CLASSIFICATION OBTA:
DATA:
CLASSIFICATION OBTA:
CLASSIFICATION DATA:
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CLASSIFICATION DATA:
DEFICE APPLICATION DATA:
DEFICE APPLICATION DATA:
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Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation STREET: 51 University Street
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US-09-871-856-13
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; ORGANISM: Drosophila melanogaster
US-09-813-329-7
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09871856 Patent No. US20020081720A1 GENERAL INFORMATION:
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TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 TLQDLQL 79
                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                   STATE: WA
                                                                                                                                                                                                                  CITY: Seattle
                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                ZIP: 98101
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Pred. No. 7e-15;
Pred. No. 7e-15;
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RESULT 8
US-10-017-910-2
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COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
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APPLICATION NUMBER: 08/996,139
EILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                               Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILI
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 317 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack
                                                                                                                                                                                                                                                STATE: New Jersey
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APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-2
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200

PRIOR APPLICATION DATA:

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RESULT 10
US-09-817-650-11
; Sequence 11, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SOFTWARE: PatentIn version 3.0; SEQ ID NO 14; LENGTH: 160; TYPE: PRT; ORGANISM: Mus musculus US-09-779-050A-14
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US-09-779-050A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RECEPTOR FROM THE FAMILY FILE REFERENCE: A-570B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOYLE, WILLIAM APPLICANT: HSU, HAILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 IPSGS---HKVSLSSWYHDRGWGKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 ATEYLOL 166
                                                                                                                                                                                                                                                                                                                                77 DYLQL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                   75 QDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                            Jacal Similarity 55.4%; es 36; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TLQDLQL 79
                                                   CORRESPONDENCE ADDRESS:
                                                                Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                              APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
CITY
                  ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 245 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
 Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%;
58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 176; DB 9;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 176.5; DB 9;
Pred. No. 1.6e-14;
4; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2:
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-877-650-11
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US-09-871-856-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206)587-04
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 DYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 SIPSGSHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,633
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 QDLQL 79
                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.

SOFTWARE: Microsoft Word for Power Macintosh

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
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APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001
                                                                                                                                                                          COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                    STATE: WA
                                                                                                                                                                                                                                         CITY: Seattle
                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 294 amino acids TYPE: amino acid
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/877,650
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Maraskovsky, Eugene
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Pred. No. 2.3e-14;
6; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                              6.0.1
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US-09-871-856-11
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US-10-017-910-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
                                                        ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/447,035

APPLICATION UMBER: US 09/447,035

APPLICATION UMBER: US 09/447,035

APPLICATION IMPORMATION:

APPLICATION IMPORMATION:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: US 09/447,035

APPLICATION UMBER: US 09/447,035

APPLICATION UMBER: US 09/447,035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 QDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 38.7%; Local Similarity 55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Josien, Regis
Steinman, Ralph
Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/996,139 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 294 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wong, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 176; DB 10; Length 294; Pred. No. 2.3e-14; 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                      ; Sequence 5085, Application US/09815242
                                           US-09-815-242-5085
                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 DYLQL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                 57 EYLQL 61
                                                                                                                                                                          75 QDLQL 79
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; TYPE: PRT; ORGANISM: Homo Sapien US-09-911-777-8
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/911,777
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BIOGEN, INC.
APPLICANT: BROTECH S.A.
APPLICANT: BROWNING, Je
APPLICANT: AMBROSE, Chr
APPLICANT: MACKAY, Fabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 8, Application US/09911777
Patent No. US20020037852A1
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use TITLE OF INVENTION: in the Modulation of B-Cell Response FILE REFERENCE: A070 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                       15 IPSISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTL 74
15 IPSGS---HXVSLSSWYHDRGWGKISNM-----YANICFRHHETSGDLAT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BROWNING, Jeffrey
AMBROSE, Christine
MACKAY, Fabienne
TSCHOPP, Jurg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 316 amino acids
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHNEIDER, Pascal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APOTECH S.A.
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.7%;
                                                                                                               25.3%; Score 115; DB 10; Length 109; 43.1%; Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibitors Thereof and Their Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 176; DB 9;
pred. No. 2.5e-14;
                                                                                                 Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 316;
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                                                                                                            Gaps
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Patent No. US20020061569A1 GENERAL INFORMATION:

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APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Wanner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
FILE REFERENCE: MSUA1-453
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/924,841
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID MOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: XU, H. HOWATG
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5085
LENGTH: 813
TYPE: PRT
ORCANISM: Decidomonas actuationsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-924-841-5
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US-09-815-242-5085
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09924841
Patent No. US20020127633A1
GENERAL INFORMATION:
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     ORGANISM: Artificial Sequence
                                           TYPE: PRT
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                771 LGIQNL 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   711 TAYLQYKEDADWNNRLQATFFDSKDYRLDGVESFGRRQVSTYTTVDLVSQYRITPDDQLS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 LTLQDL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 TSLSSWKHDQDWANVSNMTFSNGK-LRVKGI-----YYRNADICSRHRVT---SAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind, Judith W. Wall, Daniel Trawick, John D. Carr, Grant J. Yamamoto, Robert T. Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 63.5; DB 10; Length 813; 28.8%; Pred. No. 7.4; rative 11; Mismatches 23; Indels 13
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                                                                                                                                                Best Local Similarity 24.0 Matches 18; Conservative
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: modified IPNS NAME/KEY: MUTAGEN LOCATION: (210)
OTHER INFORMATION: Glu210 in native IPNS modified to Arg
115 PMIAAGTPMHEVNLW 129
                                    66 RVTSAGLTLQDLQLW 80
                                                          55 LODVVNEFHGAMTDOEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDH 114
                                                                                             15 IPSISHEAHKTSLSSWKHD------QDWANVSNMTFS--NGKLRVKGIYYRNADICSRH 65
                                                                                                                                      13.5%; Score 61.5; DB 10; Length 24.0%; Pred. No. 4.1; ative 12; Mismatches 36; Indels
                                                                                                                                                                            Length 329;
                                                                                                                                   9; Gaps
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Search completed: December 8, 2002, 19:36:15 Job time: 13.9097 secs

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
Result
                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                               Published_Applications_Na:*

1: /cgn2_6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptcdata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptcdata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptcdata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

11: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

16: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

17: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

18: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

19: /cgn2_6/ptcdata/2/pubpna/US09_NEW_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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204
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Query
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                                                                       SUMMARIES
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29.4 29.4	30	31.2	31.2	31.2	31.2	31.2	31.2	61	80.8	80.8	80.8	93.2	96.4	96.4	194	194	204	Score
14.4 14.4	14.7	15.3	15.3	15.3	15.3	15.3	15.3	29.9	39.6	39.6	39.6	45.7	47.3	47.3	95.1	95.1	100.0	Match I
409 454	30	3073	3073	3073	985	985	493	61	2237	1630	1630	1823	954	954	2412	1186	1161	Match Length DB
10	10	12	10	10	12	10	9	10	9	10	9	9	10	Q	10	10	10	
US-09-783-590-1953 US-09-864-761-14164	US-09-880-457-8	US-10-033-528-1690	US-09-920-300A-1690	US-09-867-701-10910	US-10-033-528-1691	US-09-920-300A-1691	US-10-040-739-93	US-09-880-457-9	US-10-017-910-3	US-09-871-856-10	US-09-877-650-10	US-10-017-910-1	US-09-871-856-12	US-09-877-650-12	US-09-880-457-2	US-09-880-457-3	US-09-880-457-1	ID
Sequence 1903, Ap Sequence 14164, A	α, Α Α		Sequence 1690, Ap		Sequence 1691, Ap	•	Sequence 93, Appl	Sequence 9, Appil	Sequence 3, Appli	Sequence 10, Appl	Sequence 10, Appl		Sequence 12, Appr	Sequence 12, Appl	-	•	Sequence 1, Appli	Description

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27 27 27	27.2	27.2	27.6	27.6	27.6	27.6	27.6	27.6	27.6	27.6	27.6	27.8	27.8	27.8	28.2	28.2	28.2	28.2	28.2	28.2	28.6	28.6	29.4
13.2 13.2 13.2	13.3		13.5	-						5	თ	თ	o	6	13.8	13.8	13.8	13.8	13.8	13.8	14.0	14.0	14.4
27 280 9542	2000	817	1873	1873	909	608	809	608	608	809	371	465237	2048	666	2000	477	477	477	477	477	1365	1365	2244
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US-09-880-45/-/ US-09-294-093B-5098 US-09-764-847-1809	US-09-938-842A-4387	US-09-809-545A-7	US-09-834-975-757	US-09-834-975-756	US-09-935-943-7	US-09-115-453-193	US-09-822-827-193	US-09-030-606-193	US-09-780-669-193	US-09-759-143-193	US-09-834-975-285	US-09-933-267A-1	US-09-764-847-1468	US-09-764-864-590	US-09-938-842A-4251	US-09-115-453-92	US-09-822-827-92	US-09-030-606-92	US-09-780-669-92	US-09-759-143-92	US-09-815-242-8196	US-09-815-242-4243	US-09-764-864-153
Sequence 5098, Ap Sequence 1809, Ap	Sequence 438/, Ap	Sequence 7, Appli	Sequence 757, App											sequence 590, App	Sequence 4251, AP	Sequence 92, Appr	2 2	2 2	,) L		153

ALIGNMENTS

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OY 181 TGGTGTAATTTGAGAATCATTCAC 204	OY 121 GACATTTGCTCTCGACATCGGGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTA	Qy 61 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCC	QY 1 CATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTC	Query Match 100.0%; Score 204; DB 10; Length 1161; Best Local Similarity 100.0%; Pred. No. 1.5e-60; Matches 204; Conservative 0; Mismatches 0; Indels 0;	RESULT 1 US-09-880-457-1 US-09-880-457-1 Sequence 1, Application US/09880457 Patent No. US20020106728A1 GENERAL INFORMATION: APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANTI Wood, William I. TITLE OF INVENTION: NG4 Nucleic Acids and Polypeptides and Methods TITLE OF INVENTION: for the Treatment of Body Weight Disorders FILE REFERENCE: P2871R1 CURRENT APPLICATION NUMBER: US/09/880,457 CURRENT FILING DATE: 2001-06-12 PRIOR APPLICATION NUMBER: US 50/212,901 PRIOR APPLICATION NUMBER: US 50/212,901 PRIOR FILING DATE: 2000-06-20 SEQ ID NO 1 LENGTH: 1161 TYPE: DNA ORGANISM: Homo sapiens
	180 722	120	602	Gaps	of U
	20	0			Use

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                                                                                                                                                                                   : NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: Homo sapiens
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-3
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-880-457-3
                                                                                          Matches
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                         FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09880457 Patent No. US20020106728A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09880457 Patent No. US20020106728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.

TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
684 TGGTGTAATTTGAG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TGGTGTAATTTGAG 194
                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 CATGAGGCTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGGAATGCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 95.1%; Score 194; DB 10; Length 1186; Local Similarity 100.0%; Pred. No. 4.2e-57; es 194; Conservative 0; Mismatches 0; Indels 0
                                                                                          194;
                                                                                                           Similarity
                                                                                          Conservative
                                                                              95.1%; Score 194; DB 10; Length 2412; 100.0%; Pred. No. 5.6e-57; tive 0; Mismatches 0; Indels 0
                                                                                  0;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2021 TGGTGTAATTTGAG 2034
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           SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                       FEATURE:
                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTGTAATTTGAG 194
                                    LOCATION:
                                                                                  CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                  NAME/KEY: CDS
                                                                                                       LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                       LENGTH: 954 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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Sequence 12, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                            TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      711 ACTA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
               ORIGINAL SOURCE:
                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
                                        ANTI-SENSE: NO
                                                           HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/996,139
                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                   LENGTH: 954 base pairs
                                                                                                                                                                                                                                                   TELEPHONE: (206)587-0430
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laurent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10017910 Patent No. US20020159970Al GENERAL INFORMATION:
            TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 GCTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TGAGGCTCATAAAACGAGTCTTTCTTCGTAGAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi, Yongwon Wong, Brian
                                                                                                                                                                                APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                       REFERENCE/DOCKET NUMBER: 600-1-200 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
LENGTH: 1823 base pairs
                                                                           TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Josien, Regis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 1.4e-23;
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US-09-877-650-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 TGCCGACATTTGCTCTCGACATCGCGTTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495 ACTA 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTGGGGGTAAGATCTC 374
                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997
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                 NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOPTWARE: Microsoft Word for Power MacIntosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-2001
                                                                                   APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATASKOVSKY, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
_ TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation STREET: 51 University Street
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STRANDEDNESS: double
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunex Corporation, Law Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93.2; DB 9;
Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1823;
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US-09-871-856-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-877-650-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ACATTIGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
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           APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M.
Galibert, Laurent
TITLE OF INVENTION: Receptor Activator of NF-KappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LIBRARY: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                         APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
NAME: Perkins, Patricia Anne
                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                             STATE: WA
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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REFERENCE/DOCKET NUMBER: 2851-A

REGISTRATION NUMBER: 34,693

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10017910 Patent No. US20020159970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
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Local Similarity 70.2%;
es 125; Conservative
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                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patenth Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC AC
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA
APPLICATION NUMBER: US 09/447,035
                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                      STATE: New Jersey
                                                                                                                                                                                                                                                                           CITY: Hackensack
                                                                                                                                                                                                                                                                                         STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 3..884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: <Unknown>
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                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 9
SEQ ID NO 9
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09880457 Patent No. US20020106728A1
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT APPLICATION NUMBER: US/09/880,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                         OTHER INFORMATION: Cloning oligonucleotide
                                                                                                                                                                                                                                            LENGTH: 61
TYPE: DNA
                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
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                  75 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCG 134
                                                                                                    Local
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1 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCG 60
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LOCATION: 142..1092
SEQUENCE DESCRIPTION: SEQ ID NO:
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HYPOTHETICAL: NO
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                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-11-22
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.6%;
70.2%;
                                                                           29.9%; Score 61; DB 100.0%; Pred. No. 6. tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 80.8; DB 9;
Pred. No. 4.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                DB 10; I
. 6.5e-12;
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                                                                             0;
                                                                                                                   Length 61;
                                                                             Indels
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                                                                           Gaps
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DP GA

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135

A 135

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TOPOLOGY: Tinear

HOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-040-739-93
US-09-920-300A-1691
y Sequence 1691, Application US/09920300A
patent No. US20020136728A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      377 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AAACAACGAGCCAAGCTCCAGAAAATGTTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 376
                                                                                                                                                                                                                                                                                                                                                                                                    71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
RMATION FOR GET TO TO TO THE TO 
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APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                    CTTTCAGCAACAGAAAACTAAGAGTCAAAAGGCATTTATTACCGGAATTGCCGACATT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 493 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
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APPLICANT:

Harlocker, Susan L.

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APPLICANT: Meagher, Madueloun.

APPLICANT: Xu, Jiangchun

APPLICANT: Secrist, Heather

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1691

LENGTH: 985

TYPE: DNA

ORGANISM: Homo sapiens

US-09-920-300A-1691

15.3%; Score 31.2; DB 10; Length 98
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                                                                    ; Sequence 10910, Application
; Patent No. US20020132237A1
                                                                                                                   US-09-867-701-10910
                                                                                                                                      RESULT 14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1691
LENGTH: 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1691, Application Patent No. US20020131971A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 63; Conserv
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: XI, Jiangchun
APPLICANT: XI Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
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APPLICANT: Aglate, Paul A. APPLICANT: Jones, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                        447 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 502
                                                                                                                                                                                                                                                                                                  387 ANACAACGAGCCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 502
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                                                                                                                                                                                                                                71 CTTTCAGCAACGGAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 126
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                                                                                              us/09867701
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                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.2; DB Pred. No. 0.37;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-867-701-10910
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US-09-920-300A-1690
                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Homo sapiens US-09-920-300A-1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497
CURRENT APPLICATION UNMEER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10910
LENGTH: 3073
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Matches 63; Conservative (
Search completed: December 8, 2002, 19:38:04 Job time : 18.9188 secs
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1690
LENGTH: 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 1690, Application US/09920300A Patent No. US20020136728A1
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
FILE REFERENCE: 210121.547
                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1270 AAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 1329
                                                                                                                                                        71 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 126
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                                                                                                                                                                                                                                      y Match 15.3%; Score 31.2; DB 10; Length 3073; Local Similarity 54.3%; Pred. No. 0.6; hes 63; Conservative 0; Mismatches 53; Indels 0;
                                                                                                                  71 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meagher, Madeleine Joy
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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261
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                                                                                                                                                                                                                                                                                                                Published_Applications_NA: *
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Listing first 45 summaries
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_EUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                                                                                                                                                                               /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700850
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 18	17	16	15	14	13	12	c 11	10	9	8	7	6	ر ت	4	ω	2	<u></u>	Result
30.8 30.4	31.2	31.2	31.2	31.2	31.2	31.2	33	61	95.6	95.6	95.6	118	121.2	121.2	249.4	251	261	Score
11.8 11.6	12.0	12.0	12.0	12.0	12.0	12.0	12.6	23.4	36.6	36.6	36.6	45.2	46.4	46.4	95.6	96.2	100.0	Query Match
30310 53226	3073	3073	3073	985	985	493	454	61	2237	1630	1630	1823	954	954	2412	1186	1161	Query Match Length DB
10 10	12	10	10	12	10	9	10	10	9	10	9	9	10	9	10	10	10	DB
US-09-800-631-96 US-09-818-264-3	US-10-033-528-1690	US-09-920-300A-1690	US-09-867-701-10910	US-10-033-528-1691	US-09-920-300A-1691	US-10-040-739-93	US-09-864-761-14164	US-09-880-457-9	US-10-017-910-3	US-09-871-856-10	US-09-877-650-10	US-10-017-910-1	US-09-871-856-12	US-09-877-650-12	US-09-880-457-2	US-09-880-457-3	US-09-880-457-1	ID
Sequence 3, Appli		Sequence 1690, Ap			`	Sequence 93, Appl	Sequence 14164, A	Sequence 9, Appli	Sequence 3, Appli	Sequence 10, Appr	Sequence IU, Appl	Sequence 1, Appli	Sequence 12, Appl	Sequence 12, Appl		Sequence 3, Appli	-	Description

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45	43	42	41	40	39	38	37	36	ω G	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21	20
	27.6		•	27.8	27.8	28	28	28.2	28.2	•	28.2		•	•	28.6	28.6	28.6		28.8	29.4	29.4	29.6	30	30.2
	10.6	. 7	. 7	10.7	10.7	10.7	10.7	10.8	10.8	10.8	10.8	10.8	10.8	11.0	11.0	11.0	11.0	11.0	11.0	11.3	11.3		11.5	11.6
608	371 486	465237	2222	2147	666	932	398	2000	477	477	477	477	477	1365	1365	407	357	143068	257	2244	409	2048	30	2000
10	10	10	9	9	10	10	10	9						10	10	10	10	10	10	10	10	10	10	10
us-09-759-143-193	US-09-834-975-285 US-09-783-590-10438	US-09-933-267A-1	US-09-981-353-76	US-09-981-353-104	US-09-764-864-590	US-09-925-300-515	US-09-983-965-5848	US-09-938-842A-4251	US-09-115-453-92	US-09-822-827-92	US-09-030-606-92	US-09-780-669-92	US-09-759-143-92	US-09-815-242-8196	US-09-815-242-4243	US-09-878-574-3146	US-09-878-574-3028	US-09-967-768A-316	US-09-878-574-7063	US-09-764-864-153	US-09-783-590-1953	US-09-764-847-1468	US-09-880-457-8	US-09-887-576-151
Sequence 193, App	Sequence 10438, A	٦ ٦ ٦ ٦	9	104	(U	Sequence 515, App	Sequence 5848, Ap	Sequence 4251, Ap		200		2 2	Sequence 92, Appi	8 2	4243,	3146,	Sequence 3028, Ap	Sequence 316, App		Sequence 153, App	1903,	1400,		Sequence 151, App

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-880-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09880457 ; Patent No. US20020106728A1
                                                                                                                                                                                                               Qy
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                                                                                                                                                                        Вþ
  밁
                                        δÃ
                                                                                     Дb
                                                                                                                                                                                                                                                                                                                             ucry match 100.0%; Score 261; DB 10; Best Local Similarity 100.0%; Pred. No. 1.6e-77; Matches 261; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
FILE REFERENCE: P2871R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                       666 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 725
                      181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 240
                                                                                                         121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC 180
                                                                                     AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC 665
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length 1161;
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241 TGTAATTTGAGAATCATTCAC 261

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US-09-880-457-2
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US-09-880-457-2
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TYPE: DNA

ORGANISM: Homo sapiens

US-09-880-457-3
                   SEQ ID NO 2
LENGTH: 2412
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-880-457-3
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09880457
Patent No. US20020106728A1
                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                               APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.

TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09880457 Patent No. US20020106728A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TGTAATTTGAG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       567 AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     687 TGTAATTTGAG 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 TGTAATTTGAGAATCATTCAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACCATCATCAATATCCCAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.2%; Score 251; DB 10; Length 1186; 100.0%; Pred. No. 3.6e-74; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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US-09-877-650-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                     TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2024 TGTAATTTGAG 2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1844 GAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TGTAATTTGAG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
MOLECULE TYPE: CDNA
                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, Dirk M.
                                TYPE: nucleic acid
STRANDEDNESS: single
               TOPOLOGY: linear
                                                                                                                                                                                               NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                  LENGTH: 954 base pairs
                                                                                                                                              TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/877,650 FILING DATE: 08-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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99.6%;
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ORIGINAL SOURCE:

ANTI-SENSE: NO HYPOTHETICAL: NO

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US-09-877-650-12
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US-09-871-856-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09871856 Patent No. US20020081720A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713 TA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATAICCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATASKOVSKY, BUGENE
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: (Unknown)
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181;
                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                  STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                         APPLICATION NUMBER: 08/996,139 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                             ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 121.2; DB 9; Length 954; Pred. No. 7.2e-31;
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                                                                                                                                                                                                                                                                                                                                       US-10-017-910-1
Sequence 1, Application US/10017910
Patent NO. US20020159970A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTACTATTAATGCCACCGACATCCCATCTG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ACATGACTITCAGCAACGGAAAACTAAGAGTCA----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 46.48;
Local Similarity 74.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                 TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi, Yongwon
                                                                                                                                                                                    NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181;
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REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206)587-0430
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: huRANKL (full length)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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                                                                                              STATE: New Jersey
                                                                                                                  CITY: Hackensack
                                                                                                                                 STREET: 411 Hackensack Avenue, 4th Floor
                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                        Steinman,
                                                                                                                                                                                                                                                                                                             Wong, Brian
                                                                                                                                                                                                                                                                                      Josien, Regis
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                                                                                                                                                                                                                METHODS OF USE THEREOF
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RESULT 7
US-09-877-650-10
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                                                                                                                                                                                                                             Sequence 10, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                     497 TA 498
                                                                                                                                                                                                                                                                                                                                                                                                                             122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                           236 TA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTGGGGTAAGATCTCCA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACCATCCCATCTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 45.2%; Score 118; DB 9; Length 1823; Local Similarity 74.0%; Pred. No. 1.1e-29;
                                                                                                                            Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1823 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                 STATE: WA
                                                       ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001 CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                   Galibert,
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0; Mismatches
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; Sequence 10, Application US/09871856
                          US-09-871-856-10
                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206)587-0430 TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 10:
                                                                                                         645 CT 646
                                                                                                                                            235 CT 236
                                                                                                                                                                 585 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 644
                                                                                                                                                                                      175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                                                                                                                                                                                                                           525 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC
                                                                                                                                                                                                                                                                  121 AACATGACTTTCAGCAACAGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                                                                                                                                                                                                                                                        465 GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                                                                  405 GGCAAGCCTGAGGGCCAGCCATTTGCACCACCATCAATGCTGCCAGCATCCCATCG 464
                                                                                                                                                                                                                                                                                                                                                           63 GG--CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCCATCAATATCCCCATGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-Jun-2001 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 3..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: RANKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/995,659 FILING DATE: 1997-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.6%; Score 95.6; DB 9; Length 1630; 68.2%; Pred. No. 3.2e-22;
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Best Local Similarity
                                                                                                                                                                                                                                    Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020081720A1 GENERAL INFORMATION:
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        525
                                    121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAAT 174
                                                                                  465
                                                                                                                                                          405
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FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)533-0644
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M
                                                                                                                GG--CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                    GGCAAGCCTGAGGCCCAGCCATTTGCACCACCATCAATGCTGCCAGCATCCCATCG 464
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                                                                            GGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCT 524
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 3...
                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: RANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/871,856 FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98101
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Pred. No. 3.2e-22;
0; Mismatches 69;
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NAME/KEY: CDS;
LOCATION: 142..1092;
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-017-910-3
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US-10-017-910-3
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Patent No. US20020159970A1
GENERAL INFORMATION:
APPLICANT: Choi, Yongwon
                                                                                   Matches
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
610 GGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCG 669
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                                                                                                       Local
                         3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACCATCAATATCCCATGA 62
                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                   165;
                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack
                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                 Conservative
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Wong, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Josien, Regis
                                                                                                36.6%;
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                                                                               Score 95.6; DB 9;
Pred. No. 3.7e-22;
0; Mismatches 69;
                                                                                                                   Length 2237;
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; Sequence 14164, Application US/09864761
; Patent No. US20020048763A1
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US-09-880-457-9
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LENGTH: 61
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Best Local Similarity
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                                                                                                                                                APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR EILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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ORGANISM: Artificial Sequence
FEATURE:
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| CT 851
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100.0%;
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. 2.7e-11;
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RESULT 12
US-10-040-739-93
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                                                                                                                                         Sequence 93, Application US/10040739 Patent No. US20020173635A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax
SEQ ID NO 14164
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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PRIOR
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 454
                                                                                                                                                                                                                                                             309
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                             APPLICANT:
NUMBER
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                                                                                                                                                                                                                                                                                            TTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTA 201
                                                                                                                                                                                                                                                                                                                            GAGATTGTGGAGGCAAATACATTCTCACAAACTGCTGTTGGAAACATAATATGTATATTT 310
                                                                                                                                                                                                                                                                                                                                                                                             81;
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          Merberg, David
Treacy, Maurice
Spaulding, Vikki
OF INVENTION: SECRETED,
OF.
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SEQUENCES:
                                                                                                                            Jacobs, Kenneth
                                                                                             McCoy, John
LaVallie, E
                                                                              Racie, Lisa
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Pred. No. 0.15;
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               EXPRESSED SEQUENCE TAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 454;
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APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SED ID NOS: 1789
SEQ ID NO 1691
LENGTH: 985
TYDDF: DNA
                                                                                           US-09-920-300A-1691
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US-09-920-300A-1691
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        Matches
                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1691, Application US/09920300A Patent No. US20020136728A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 183
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 ATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA 127
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MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
        63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
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      Conservative
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                          12.0%;
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54.3%;
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Score 31.2; DB Pred. No. 0.83; 0; Mismatches
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                                           DB 10;
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    53;
                                           Length 985;
    Indels
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Gaps
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APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: RND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT EILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10910

LENGTH: 3073

TYDE: DNA

ORGANISM: Homo sapiens

US-09-867-701-10910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: U$/10/033,528
CURRENT APPLICATION NUMBER: U$/10/033,528
CURRENT APPLICATION NUMBER: U$/12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1691
LENGTH: 985
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-528-1691
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                                                                                                 Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10910, Application US/09867701 Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1691, Application US/10033528 Patent No. US20020131971A1
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1270 AAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGAAATT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 183
                       68 ATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA 127
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                                                                                                                Match 12.0%;
Local Similarity 54.3%;
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Local Similarity 54.3%;
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Meagher, Madeleine Joy
                                                                                               Conservative
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                                                                                             0;
                                                                                                                Score 31.2; DI
Pred. No. 1.4;
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Search completed: December 8, 2002, 19:37:57 Job time: 24.2491 secs

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OM nucleic - nucleic search, using sw model
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score greater than or equal to the score of the result being printed,
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1 aaaagaggataattcaagaa.....taataaaaggaggaaaatgc 1161
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100.0 1161

35.5 2412

23.1 1186

10.9 954

10.6 1823

8.4 1630

8.4 2237

5.3 180216

3.3 187997

3.1 37097

3.1 37097

3.1 370

3.1 12259

3.0 12259

3.9 517161
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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(Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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3. (Cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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US-09-867-701-10680

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Sequence 3, Appl
Sequence 12, Appl
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Sequence 6187, Ap
Sequence 10680, A
Sequence 1690, Ap
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Sequence 10, Appl
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s and Methods of Use				3950,	529,	292,	469,	440,	595,	245,	45,	sequence 245, App				Sequence 3727, Ap								199	141	14	۲,	·w	

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-880-457-1
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CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                       Matches 1161; Conservative
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/212,901 PRIOR FILING DATE: 2000-06-20
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121 AAGGACGTGGTTGCGAGGACATGGAGGAAAGTTCTACAGAGGAGGAGCACAGTGGGCTTCA 180
121 AAGGACGTGGTTGCGAGGACATGGAGGGAAAGTTCTACAGAGGAGGCACAGTGGGCTTCA 180
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Patent No. US20020106728Al
GENERAL INFORMATION:
APPLICANT: Pan, James
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Goddard, Audrey
Wood, William I.
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CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 2412
TYPE: DNA
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                                                      1875 AACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAG
                                                                                                                                                                           1695 GGACACTGAAGGTGTATCGTTGGCCCTGCCAGCTGCAAGTGAACTGCTTCTGATGAATTT 1754
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                                                                                                                                                577 AACATGACCAAGATTGGGCAAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAG
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GCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATTTGAG 2034
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-3
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CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use TITLE OF INVENTION: for the Treatment of Body Weight Disorders
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APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
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                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTT 648
                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACCTTCAGCTATGGTGTAATTTGAG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268;
                                APPLICATION NUMBER: US/09/877,650 FILING DATE: 08-Jun-2001 CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                       ZIP: 98101
                                                                                                                                                                                                                                                                  STATE: WA
APPLICATION NUMBER: 08/995,659
                                                                                                                                                                                                                                                 COUNTRY: USA
                   APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.1%; Score 268; DB 10;
100.0%; Pred. No. 3.1e-76;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                   Sequence 12, Application US/09871856; Patent No. US20020081720A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                  US-09-871-856-12
                                                                                                                                                                                                                                                                                                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                                                                    689 ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                         697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 10.9%;
Local Similarity 72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                            TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206)587-0430
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                     STATE: WA
                                         CITY: Seattle
                                                          STREET: 51 University Street
COUNTRY: USA
                                                                             ADDRESSEE: Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE:
                                                                                                                                                           Galibert, Laurent
Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO
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pred. No. 2.2e-30;
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; Sequence 1, Application US/10017910
; Patent No. US20020159970A1
                                             RESULT 6
US-10-017-910-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                     689
                                                                                                                                                                    697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                             640 ---AAGGCATTTACTGCGAATGCCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                          569 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 628
                                                                                                                                                                                                                                                                                                                   583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACCTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                                              509 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                                                                                                                    525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                         AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 688
                                                                                                                            ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: PERKINS, PATRICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: huRANKL (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126; DB 10;
Pred. No. 2.2e-30;
0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 954;
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                                                                                                                                                                                                                                                                                                                                                                 Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1823 base pairs
                               413 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG 472
697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                  640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                              353 ATCGGGGGTGGGGTAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                   583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                 525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                          293 TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                                       233 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 292
                                                                                                                                                                                                                                                                                                           465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wong, Brian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201-343-1684
                                                                                                                                                                                                                                                                                                                                                                         10.6%; Score 122.8; DB 9 71.8%; Pred. No. 3.6e-29;
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                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                            Length 1823;
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US-09-877-650-10
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                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-877-650-10
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                    Query Match
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                                                                                                                        477 TIGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCA 536
537 ATATCCCATGAGG--CTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGG 594
                                                               394 TGGCCCAGCGAGGCAAGCCTGAGGCCAGCCATTTGCACACCTCACCATCAATGCTGCCA 453
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Galibert, Laurent
Galibert, Laurent
Galibert, Laurent
Galibert, Laurent
Galibert, Caurent
Galibert, Ca
                                                                                                                                                                                                                         Local Similarity
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MEDIUM TYPE: Floppy disk
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                           170; Conservative
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/877,650 FILING DATE: 08-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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STRANDEDNESS: single
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LOCATION: 3..8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (206)233-0644
                                                                                                                                                                                                                      8.4%;
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                                                                                                                                                                                           Score 97; DB 9; Length 1630; Pred. No. 7.3e-21; 0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
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                                                                                             FEATURE:
                                                                                                                                                                                        IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
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FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

FILING DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                 NAME/KEY: CDS
LOCATION: 3..884
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                                                                                                                        CLONE: RANKL
                                                                                                                                                             LIBRARY:
                                                               NAME/KEY:
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US-10-017-910-3
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                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Local Similarity 67.2%;
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ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAMETHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Choi, Yongwon
Wong, Brian
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STRANDEDNESS: double
                 TYPE: nucleic acid
                                                                                                           TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                   LENGTH: 2237 base pairs
                                                                                             TELEX: 133521
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/447,035 FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Avenue, 4th Floor
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Pred. No. 7.3e-21;
0; Mismatches 75; Indels
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Best Local
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 9
SEQ ID NO 9
LENGTH: 61
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09880457 Patent No. US20020106728A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR LING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pan, James
                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 170; Conservative
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                                                                                                                                                                                                                                                                                FEATURE:
                                                                          677 A 677
                   61 A 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              649 ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 CCAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCT·778
                                                                                                                                                        Match 5.3%; Score 61; DB 10; Local Similarity 100.0%; Pred. No. 3.6e-10; es 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       709 AGGACCTTCAGCT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 CAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             659 GCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGG 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537 ATATCCCATGAGG--CTCATAAAAGGAGTCTTTCTTCGGAAACATGACCAAGATTGGG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     599 TGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
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Pred. No. 9.1e-21;
0; Mismatches 75; Indels
                                                                                                                                                                                           Length 61;
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US-09-835-232-6/c
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NAME/KEY: misc_feature

LOCATION: (1)...(180216)

OTHER INFORMATION: n = A,T,C or G

US-09-835-232-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 124718 AAGCACCTACTAAGTACCAGGCACTATTTGGGATGTGGGGGACACAACAAGAGGAAAAACT 124659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09835232
Patent No. US20020098489A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 124598 AGGCAACCAAATGC 124585
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APPLICANT: Leder, Benjanin
APPLICANT: Leder, Benjanin
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
FILE REFERENCE: 00383/052002
CURRENT APPLICATION NUMBER: US/09/835,232
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/196,811
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
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LENGTH: 180216
                                                                                                                                              US-09-822-246-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09822246 Patent No. US20020142383A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 197997
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TILE REFERENCE: CLOUI149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/822,246
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 4
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 AAGTATCTACAAGGCACCAGGCATTTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCA 406
                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(197997)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                  ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                 TYPE: DNA
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                363 CCAGGCATTTTTGAGCATTTGGGGATTTGTCAGCAAACAAGTCAGACAAAAAACCTTGCT 422
                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74; Conservative
h 3.3%; Score 38; DB 10; Length 197997; Similarity 65.1%; Pred. No. 2.1; 56; Conservative 0; Mismatches 30; Indels 0;
       0; Mismatches
           30; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6187, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
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SEQ ID NO 6187
LENGTH: 370
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APPLICANT: Aglate, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                            US-09-867-701-10680
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FULE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 110912

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 10680
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patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 CTGGTGGAGGGAACATTCTAGCAAAG 448
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: HARLOCKER, SUSAN L.
APPLICANT: HARLOCKER, SUSAN L.
APPLICANT: HARLOCKER, SUSAN L.
APPLICANT: ANY DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                       LENGTH: 495
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Local Similarity 62.2%;
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                                                                                                                                                            715 TTCAGCTATGGTGTAATTTGAGAATCATTCACTGAGCATCAACTATGTAACCAGCATTGG 774
                                                                          775 GTTGGGTGCCAGAGATCCAAAGCTAAGACA 804
                                                                                                                                                                                                                                Local
                                   65 GTTAGGTCCCACACATACAGAGCTGAATCA 94
                                                                                                                    5 TTCGTTCATTTATTCATTCAACAAACATTATATGAGCACCCACTATGTGCCAGGCACAGT 64
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Similarity 62.2%;
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                                                                                                                                                                                                                  Score 35.6; DB 10; Length 495;
pred. No. 0.24;
0; Mismatches 34; Indels 0
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0;

Matches Query Match

TYPE: DNA

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0; Gaps

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US-09-764-869-1690/c

Sequence 1690, Application US/09764869

Patent No. US20020061521A1

APPLICANT: ROSEN et al.

PILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

CURRENT FILE DE INVENTION: Nucleic Acids, Proteins, and Antibodies

CURRENT APPLICATION Number: US/09/764,869

PILE REFERENCE: PC007

CURRENT FILE DATE: 2001-01-19

PILE REFERENCE: PC007

CURRENT APPLICATION NUMBER: US/09/764,869

PILO APPLICATION NUMBER: US/09/764,869

PILO APPLICATION NUMBER: US/09/764,869

PILO APPLICATION OF COMMENT OF COMMENT OF COMPANY APPLICATION NUMBER: US/09/764,869

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SPTREMBL_21:*

SP_archea:*

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Sp_bacteria

Sp_fungi:*

Sp_fungi:*

Sp_human:*

Sp_human:*

Sp_mhc:*

Sp_mhc:*

Sp_mhc:*

Sp_phac

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373
1 HEAHKTSLSSWKHDQDWANV......TSAGLTLQDLQLWCNLRIIH 68
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    sp_vertebrate:*
sp_unclassified:*
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sp_human:*
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10000000000000000000000000000000000000	Result
69 69 64.5 64.5 63.5 63.5 62.63	Score
18.5 18.5 18.2 18.0 18.0 17.3 17.3 17.3 17.3 17.3 17.3 17.3 17.3	% Query Match Length
214 1130 187 296 307 478 276 1000 1018 1090 1214 297 2813 2813 285 166	
13 13 15 10 11 11 11 11 11 11 11 11 11 11 11 11	DB
Q9DDZ5 Q88282 Q88282 Q9FGA8 Q9FGA8 Q9FT49 Q71146 Q71130 Q71130 Q9I189 Q9U189 Q9U189 Q9Y6M7 Q9	SUMMARIES ID
Ogdaz5 brachydanio O88282 snakehead r O9fga8 arabidopsis O9x297 thermotoga O9ff49 arabidopsis O971146 human immun O97130 clostridium O97130 clostridium O90159 homo sapien O960350 homo sapien O960350 homo sapien O960350 homo sapien O90607 homo sapien O90607 homo sapien O90759 drosophila O913x9 pseudomonas O90wt9 gallus gall O942bl oryza sativ O96zt5 sulfolobus	Description

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1514	1514	830	729	425	391	262	646	330	308	1171	316	237	91	364	187	427	261	216	216	156	2353	609	354	274	1630	1101	530	322
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Q9VUNO	Q9NBK9	Q99LF9	092IP3	099YE2	Q9JRL2	Q9FAC1	081015	058765	08R5Y5	097в.17	096BW9	Q9X6N2	022506	Q8RFS0	068768	Q9K9G9	Q92NK4	Q8XDI7	Q82K87	Q97516	Q8XTZ4	Q989R7	Q8UDK4	Q8YZI4	Q8RHH7	045818	Q9VFV1	Q95xD5
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ila	SCULU	CSId	streptococc	Supp	actebronivce	STSGODIGE	ccus	rusopacteri	chermoplasm	nomo sapien	actebronize actebronize	Caeriorilabut	CCCTT	yerarura pe		=	TCILLE	escherichia escherichia	SUCTOTORS	n La S			anabaena sp	TIALLOPACIETI	Caellot liabut) F	drosophila	

ALIGNMENTS

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76 HQSCRHPVHTWANKSFGAHLYNWTLTNGRLRVPQDGRYYLYSQVYFRY 123	~ ~ ~	PRELIMINARY; PRT 2001 (TrEMBLrel 16, Creat, 2001 (TrEMBLrel 16, Last 8, 2002 (TrEMBLrel 20, Last 8, 2002 (TrEMBLrel 20, Last 8, 10, Last 1	RESULT 1 Q9DDZ5

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AC DATE DO CONTROL OF 
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δõ
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Best Local
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Best Local
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Q88282; PRELIMINARY; PRT:
Q88282;
Q1-NOV-1996 (TrEMBLrel O1, Last sequence on the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hart D., Frerichs G.N., Rambaut A., Ronalds R.J., Onions D.E.; "Evidence for a new retrovirus genus of piscine origin."; submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U26458; AAC54858.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96211493; PubMed=8648695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snakehead retrovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sanotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
similarity to pollen-specific protein Bnml.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snakehead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete nucleotide sequence and transcriptional analysis snakehead fish retrovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hart D., Frerichs G.N., Rambaut A.,
                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB026650; BAB10289.1; SEQUENCE 187 AA; 20056 MW; 305781D3A0738AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 SSGNSWKAEIDKIRKQKW----QKCYFSGKLRIKGTDYEEIDTCPKPLIGPLSGFIPTGV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Katoh T., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FGA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 TKTLKTGVTWTTAVVKIDLQQWVDI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virol. 70:3606-3616(1996).
                                                                                    102 HDAYVGILASLKSALLELKDSPDTANYDVMVSGDDTRRVKGLVEKNTDTASK---TLMEM 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 GLTLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TSLSSWKHD-----QDWANVSNMTFSNGKLRVKGIYYRNADICSRHRV-----TSA 51
    54 TLQDLQL 60
                                                                                                                                                                    1 HEAH-----KTSLSSWKHDQDWANVSNMTFSNGKLRVKGTYYRNADICSRHRVTSAGL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                         18.2%; Score 68; DB 32.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 AA
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                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 187;
                                                                                                                                                                                                                                                                               26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1130;
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                                                                                                                                                                                                                                                                                        Gaps
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Q9FT49
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                 Best
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9X2G7

O9X2G7;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 20,

O1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein TM1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR, TM1852; -
Hypothetical protein; Complete proteome.
SEQUENCE 296 AA; 34197 MW; 11B3980CA5C3D2C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 TLQMEQL 165
                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Bukaryota; Viridiplantae; Streptophyta; core e

Spermatophyta; Magnoliophyta; eudicotyledons; core e

spermatophyta; Magnoliophyta; eudicotyledons; core e

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9FT49
                                                                                                                                                                                                                                                                                                                                                              Hypothetical 34.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FT49;
                                                                                             EU Arabidopsis sequencing project; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL132972; CAC07924.1;
                                                                                                                                                                                                SEQUENCE FROM N.A.

Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
                                                                                                                                                                             Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                  T25B15_100.
                                                                 SEQUENCE
                                                                                 Hypothetical protein
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 EEDWEKFGGVPNVVFSDAMIEYNGYYYVYYGAADNC----IALATIPVEKVMKWC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 DQDW---ANVSNMTFSNGKLRVKG---IYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE001822; AAD36914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
 Conservative
                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.0%; Score 67; DB 1 27.3%; Pred. No. 3.1; tive 11; Mismatches
                   18.0%;
18.3%;
                                                                   34863 MW; DC8746CB47D8F92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                   Score 67; DB Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 AA
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                                       DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                       update)
        26;
                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
                                      Length 307;
        Indels
                                                                                                                                                                                                                                                                                                                          Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
            22;
                                                                                                                                                                                                                          Rudd
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            Gaps
            2
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Matches

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RESULT 6
Q71146
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Query Match
Best Local
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q71146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quinones-Mateu M.E., Dopazo J., Este J.A., Rota T.R., Domingo E., "Molecular characterization of human immunodeficiency virus type 1 solates from Venezuela."; ALDS Res. Hum. Retroviruses 11:605-616(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Envelope glycoprotein gp120 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 AWIDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96093896; PubMed=7576917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 ADICSRHRVTSAGLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E., "Point mutant frequencies in the pol gene of human immunodeficiency virus type 1 are two- to threefold lower than those of env."; virus type 1 are two-to threefold lower than those of env."; AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDS Res. Hum. Retroviruses (EMBL; U16766; AAC55683.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS;
                                                                                               01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-
                                                                                                                                                                                                                                                                                                                                                                                                             128 SFNITTSSGEKMQKEALFYNLDVV 151
                      Bacteria; Firmicutes; Bacillus/Clostridium Clostridiales; Clostridiaceae; Clostridium
                                                                           Clostridium acetobutylicum
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 SRHRVTSAGLTLQDLQLWCNLRII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 OMHEDIISLW--DOSLKPCVKLTPLCVTLDCTDWGNATNTNISSGGAMERG----EIKNC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EAHKTSLSSWKHDQ------DWANVSNWTFSNGKLRVKGIYYRNADIC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%; Score 67; DB illarity 25.0%; pred. No. 5.5; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53554 MW; 103F636765B51D92 CRC64;
                                                          Bacillus/Clostridium group; Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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RESULT 8
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                                                                                                                                      RESULT 9
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 Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007588; AAK78712.1;
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09UIB9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        о9иів9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 NWK-DESWIDVSNLKWDNYVVNTLGKNLKNKGVDGFFLDNLDVYSKYKKDSMFIGLLNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Romero M.F.; romain brain, similar to "Cloning of a HCO3 transporter, NT2-NBC, from human brain, similar to both the Anion exchangers (AEs) and the Na/Bicarbonate Cotransporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bicarbonate transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SWKHDQDWANVSNMTFSN-----GK-LRVKGI---YYRNADICSRHRVTSAGLTLQDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF053755; AAF21720.1;
                                                                                                                                                                                                                                                                                                                                                                                         HSSP; p02730; IBNX:
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotransp.
InterPro; IPR003020; HC03_cotransp.
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO0834; ae;
                                            01-AUG-1998 (TIEMBLrel. 07, Created)
01-AUG-1998 (TIEMBLrel. 07, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
sodium bicarbonate cotransporter2.
                                                                                                                          060350
                                                                                                                                                                                                      564 TLAQWKKDNITAHNISWRNLIVSECK-KLRGVFLGSA--CGHH-----GPVIPDVLFWC 614
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                 7 SLSSWKHDQDWA-NVS--NWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                      19;
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276 AA; 32104 MW;
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                                                                                                                                                                                                                                                                                                                                  1000 AA;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                PRELIMINARY;
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30.5%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                    112501 MW;
                                                                                                                                                                                                                                                                      17.3%; Score 64.5; L
32.2%; Pred. No. 28;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
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                                                                                                                                                                                                                                                                                                                                         93FAA40A3141F8F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 AA
                                                                                                                                          1018 AA.
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                                                                                                                                                                                                                                                                                                            DB 4; Length 1000;
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                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                         11;
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Q9Y6M7
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09Y6M7
PRELIMING....

09Y6M7;
PRELIMING....

01.NOV-1999 (TREMBLrel. 12, Created)
01-NOV-1999 (TREMBLrel. 12, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
                                                                                                                                                                                      Matches
                                                                                                                                                                                                         Query Match
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                                                                                                                     654 TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GPYIPDVLFWC 704
                                                                                                                                                                                                           TIGREÀMS; TIGRO0834; ae; 1.
SEQUENCE 1090 AA; 123080 MW; 541839CC9B565896 CRC64;
                                                                                                                                                                                                                                         InterPro; IPR001717; Anion_exchange. InterPro; IPR001707; HC03_cotransp. Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                    09HC88;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sodium bicarbonate cotransporter 2b.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                            PISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                           7 SLSSWKHDQDWA-NVS--NWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                                                                                                                                                      Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       о9нсвв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GPYIPDVLFWC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; iPR001717; Anion_exchange.
InterPro; iPR003020; HC03_cotransp.
Pfam; PF00955; HC03_cotransp; 1
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blochem Biophys. Res. CommuEMBL; AB012130; BAA25898.1; HSSP; p02730; IBNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishbbashi K., Sasaki S., Marumo F., "Molecular cloning of a new sodium bicarbonate cotransporter cDNA from human retina.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 SLSSWKHDQDWA-NVS--NWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                             lia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                            Similarity
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                    Abuladze N., Newman D., Hwang J., Kurtz I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR00834; ae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1018 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                   17.3%; Score 64.5; 32.2%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 64.5; DB 4; Length 10
32.2%; Pred. No. 28;
ative 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114204 MW; A37799D93A1E30BC CRC64;
                                                                                                                                                                               12;
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                                                                                                                                                                         Mismatches
                                                                                                                                                                                       _ DB 4; Length 1090;
                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo
                                                                                                                                                                     17; Indels
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RX MEDILINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gulbart M.M., Glasser K.,
RA Harlis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison JA., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09VCJ9;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        778 TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GPYIPDVLFWC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotransp.
Pfam; PF00955; HCO3_cotransp; 1
PRINTS; PR01231; HCO3TRNSPORT.
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TIGREAMS; TIGRO834; ae; 1.
1714 AA; 136042 MW;
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Pushkin A., Abuladze N., Lee I., Newman D., Hwang J., Kurtz I.;
"Cloning, tissue distribution, genomic organization, and function characterization of NBC3, a new member of the sodium bicarbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cotransporter family.",
J. Biol. Chem. 274:16569-16575(1999).
EMBL; AF047033; AAD38322.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 62
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Q9I3X9
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Mixon K., Nusskern D.R., Pacleb J.M.,
RRA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RRA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Yenter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
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                                                                                                                                                                                    Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
Receptor; Complete proteome.
SEQUENCE 813 AA; 89127 MW;
                                                                                                           opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004565; AAG04754.1;
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01-MAR-2001 (TrEMBLrel. 16, Last
01-OCT-2001 (TrEMBLrel. 18, Last
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000169; SHprot_acsite.
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15; Conser
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297 AA; 33480 N
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34.9%;
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Pred. No. 8.6;
5; Mismatches
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3E61AB56E3105299 CRC64;
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Best Local (
clone:B1060H01.
Submitted (MAY-:
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
B1060H01.30 protein (OSJNBb0021A09.1 protein).
B1060H01.30 OR OSJNBB0021A09.1.
                                                                                                                                     Oryza sativa (Rice), and
Oryza sativa (Japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                 Sasaki T., Matsumoto
                                                               STRAIN=CV. NIPPONBARE;
                                                                                                     Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=4530, 39947;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat.
TMF-related apoptosis inducing ligand.
Gallus gallus (Chicken).
                                   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                               SEQUENCE
                                                                                                                                                                                                                                                              Q942B1
                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002012; TNF_abc; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 287 AA; 32092 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057941; AAL23702.1; .
InterPro; IPR003436; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.;
"TNF-related apoptosis inducing ligand (TRAIL) expression in
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16; Conservative
                                                                              FROM N.A.
            (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                            PRELIMINARY;
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28.8%;
                                                    Yamamoto K.;
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Pred. No. 29;
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Title:
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Gapop 10.0 , Gapext 0.5
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373
1 HEAHKTSLSSWKHDQDWANV......TSAGLTLQDLQLWCNLRIIH 68
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Database :

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ALIGNMENTS	RRPL_SV5 PIS_YEAST GUB_CLOIM PROB_MEIRU PPAL_SCHPO PRTG_ERWCH S6A7_HUMAN PAG_BACAN PAG_BACAN PO21_SCICO BGAL_LACDE YDY2_SCHPO MSH6_YEAST
	Q88434 P06197 P29716 Q9z998 P08091 Q07162 Q99884 P13423 Q03279 P20043 Q13683 Q03834
	simian viru saccharomyc clostridium meiothermus schizosacch erwinia chr homo sapien bacillus an sciara copr lactobacill schizosacch saccharomyc

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SEQUENCE FROM N.A. (ISOFORM 2). TISSUE=Tongue;	iol. Chem. 272:25190-25194(1997).	NCE is a novel ligand of the tumor necro	Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;	ubMed=9312132;	TISSUE=Thymocytes;		mitted (JUN-20	H., Hirokawa K.;	SEQUENCE FROM N.A. (ISOFORMS 1;	Cell 93:165-176(1998). [3]	differentiation and activation.";	"Osteoprotegerin ligand is a cytokine that regulates ostooglast	Kaufman S., Sarosi I., Shalhoub V., Senaldi G., G	Sullivan J., Hawkins N., Davy E., Capparelli C., Scully S., Hsu	Burgess T., Elliott R. Colombaro & Elliott G. C	MEDLINE=982	TISSUE=Lymph node;	SECULENCE EBOM N A (TECHON 1	Nature 390:175-179(1997).		"A homologue of the TNF recentor and its limits which is	Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.	Anderson D.M., Maraskovsky E., 1	MEDLINE=98032977; PubMed=9367155;	TISSUE-Bone marrow, and Perinheral blood.		NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhin: Hominidae, Lome	Fukarvota: Metazoa: Chordata Compainto Testal .		Threell of Bank of the first of	induc		Tumor	15-00	16-00	0147	TUTAN GERMANAN GERMANANAN SER	

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 269:532-536(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oy non-profit institute. There are no restrictions modified and this statement is not removed. Usage hv and or send an analysis a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20175237; PubMed=10708588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                               CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                              VARSPLIC VARSPLIC
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00229; TNF;
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                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                   Signal-anchor;
                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                              SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003636; TNF_abc
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
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                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                               PROSITE; PS00251; TNF_1; FALSE_NEG. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000478;
                                                                                             CARBOHYD
                                                                                                          CARBOHYD
                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are produced by alternative splicing.

TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEAP PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.

INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.

PTM: The soluble form of isoform 1 derives from the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and secreted (isoform 2). A soluble form of isoform 1 arises by proteolytic processing (By similarity).

ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    catalyzed by ADAM17
                                                                                                                                                                                                                                                                                                                                                                                                           602642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteolytic processing (By similarity). The cleavage may
                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:11926; TNFSF11.
                                                                                                                                                                                                                                                                                Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                       140
                                                                                             198
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139
171
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                                                                                                                                                                                                                                                   Alternative splicing
1 317 TUMOR 1
                                                                                                                                                                                                                                                                                                                                              TNF_abc; 1.
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171
198
198
47
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce,
                                   35478 MW;
                                                                                                                                                                                                                                                                                                                                                                             TNF_family.
   47.78;
                                                              CLEAVAGE (BY SIMILARITY).

"-LINKED (GLONAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).

MISSING (IN ISOFORM 3).

MISSING (IN ISOFORM 2).
                                                                                                                                                                                                       MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
      Score 178;
                                                  A -> G
                                                                                                                                                                         SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                     766176446348097F CRC64;
                                                    (IN REF
      DB 1;
                                                                                                                                                                                           (POTENTIAL)
      Length 317;
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TN11_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9ESE2; Q91ZI9;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Fischer 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marks S.C. Jr.;
"Evidence that the rat osteopetrotic mutation toothless (tl) is not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11804028;
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                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                             InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                     HSSP; P50591;
                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           entities
                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                           between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNRSFILA/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Highly expressed in thymus and bone
                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the E
                                                                                                                                        AF187319; AAG17031.1; -.
                                                                                                             AF425669;
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                                                                                                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                     1D0G.
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5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPGL) gene.";
                                                                                                                                                                                                                                                                                                                      There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                 by and
                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
                                                                                                                                                                                                                                                                                               żs
                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
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Pfam; PF00229;

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REPRESENTED TO SERVICE STREET 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00251; TNF_1; FALSE_NEG PROSITE; PS50049; TNF_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
11 (Receptor activator Tumor necrosis factor ligand superfamily member 11 (Receptor activation of nuclear factor Kappa B ligand) (RANKL) (TWF-related activation induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNII_MOUSE STANDARD; PRT; 31
035235; 035306; Q9RIYO; Q9JJK8; Q9JJK9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upd
15-JUN-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 SHKVSLSSWYHDRGWAKISNWTLSNGKLRVNQDGEYYLYANICERHHETSGSVPADYLQL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gnal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THESE 11 OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97460112; PubMed-9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIVYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                         Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                        TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANCE is a novel ligand of the tumor necrosis factor receptor family
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1)
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
                                                                     TISSUE=Bone marrow;
MEDLINE=98227661; PubMed=9568710;
                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                  Nature 390:175-179(1997)
                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD002012; TNF_abc; 1.
                                                                                                                                                                                                                homologue of the INF receptor and its ligand enhance I-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                    activates
                                                                                                                                                                                                 dendritic-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
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140
199
264
317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                  272:25190-25194(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                         function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBER 11, MEMBRANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I -> M (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4B87A4D706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasuda H., Shina N., Nakagawa N., Yamaguchi K., Kinosaki M., Mochizuki S.I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E., Mochizuki S.I., Tomoyasu A., Yano K., Takahashi N., Suda T., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T., "Osteoclast differentiation factor is a ligand for "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis inhibitory factor and is identical to TRANCE/RANKL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation and activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ofteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Bone marrow stroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ueda M., Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99214075; PubMed=10196481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kodaira K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of nuclear
factor-kappaB ligand and their differential expression in bone and
thymus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 230:121-127(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., Schloendorff J., Tempst P., Choi Y., Blobel C.P., Erdjument J., Tempst J., Choi Y., Blobel C.P., Erdjument J., Tempst J., Choi Y., Blobel C.P., Erdjument-Bromage H., Tempst P., Choi Y., Blobel C.P., Erdjument-Bromage H., Erdjumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  survival.
                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
"Crystal structure of the TRANCE/RANKL cytokine reveals determinants
of receptor-ligand specificity.";
of receptor-ligand specificity.";
J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
PubMed=11733492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.; "Crystaal structure of the extracellular domain of mouse RANK ligand at
-i- SUBCELLULAR LOCATION: Type II membrane protein and secreted
(1soforms 1 and 2); Cytoplasmic (1soform 3);
(1soforms 2) and 3; are
-i- ALTERNARIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT-
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TELLS.
NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN THE
BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                                                                 JIOI. Chem. 277:6631-6636(2002).

FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to FUNCTION: Cytokine that binds to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. TNFRSF11A/RANK. Osteoclast differentiation and incomments the ability of immovement recommendations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A resolution.";
3101. Chem. 277:6631-6636(2002).
                                                                                                                                                                                                                                                                                proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play
                                                                                                                                                                                                                                                    an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                               hypercalcemia of malignancy.
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RESULT 4
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                                                                                                                                                                                                                                                     Query Match
                178 SHKYTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00251; TNF_1; FALSE_NEG. PROSITE; PS50049; TNF_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal-anchor;
                                                                       3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00229; TNF;
SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                               loca!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this strategy are supported in the support of the support 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: N-91ycosylated.
-!- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by Proteolytic processing. The cleavage may be catalyzed by Proteolytic processing. The cleavage may be catalyzed by Proteolytic processing. The creavage may be catalyzed by Proteolytic strip of the processing of the proteolytic strip of the pr
                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:1100089; Tnfsf11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1JTZ; 12-SEP-01.
1IQA; 13-MAR-02.
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRABECULAR BONE AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differentiation; Receptor; Glycoprotein; Transmembrane; chor; 3D-structure; Alternative splicing.

1 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, MEMBRANE FORM.
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                            316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; BAA97258.1; -.
3; BAA97259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF;
                                                                                                                                                                                                        46.18;
56.78;
                                                                                                                                                                                                                                                                                                  34944 MW;
                                                                                                                                                                              6,
                                                                                                                                                                           Score 172; UB 1,
No. 4.4e-14;
                                                                                                                                                                                                                                                                                                            G -> D (IN REF. 2).
MISSING (IN REF. 5)
                                                                                                                                                                                                                                                                                                                                                                          SSEEMGSGFGVPHEGPLHPAPSAPAPAPAPPPA -> TP (IN
                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
MISSING (IN ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.
                                                                                                                                                                                                                                                                     08DF63A2BE00967A CRC64;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                     DB 1; Length 316;
                                                                                                                                                              18;
                                                                                                                                                 Indels
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ACCOCCARACTER AC
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ID PPYRE_PICAN
ID PPYRE_PI
AC Q06375;
DI 01-JUN-
DI 15-JUN-
DI 15-JUN-
DI 15-JUN-
DI 01-JUN-
DI 02-JUN-
DI 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                           MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Ev
Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable cytochrome P450 28d2 (EC 1.14.-.) (CYPXXVIIID2).
CYP28D2 OR CG6081.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                              STRAIN-Berkeley,
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VMT6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSD2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrimidine biosynthesis; Lyase; Decarboxylase.
ACT_SITE 92 92 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 DRKFADIGNTV----KLQYKGGIYRTSKWADITNAHGVTGAGI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S31323; S31323.
HSSP; P03962; IDQW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 DQDWANVSNMTFSNGKLRVKGIYYRN---ADICSRHRVTSAGL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merckelbach A., Goedecke S., Janowicz Z.A., Hollenberg C.P.; "Cloning and sequencing of the ura3 locus of the methylotrophic ye Hansenula polymorpha and its use for the generation of a deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94128354; PubMed=7764392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UN-1994 (Rel. 29, Created)
01-UN-1994 (Rel. 29, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Orotidine 5'.phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
(OMPDCase) (OMPdecase) (Uridine 5'.monophosphate synthase) (UMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRF_PICAN Q06375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00215; OMPdecase.
PF00215; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X69461; CAA49221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA; 29275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.5; DB 1; 1
Pred. No. 1.2;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0934EF673B03A820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lotrophic yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
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Abril J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Beasley E.M.,

Ra Ballew R.M., Basen A., Bayraktaroglu L., Beasley E.M.,

Ra Beeson K.Y., Berman B.P., Bhandari D., Bolshakov S.,

Ra Beeson K.Y., Berman B.P., Bhandari D., Bolshakov S.,

Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Ra Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Ra Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,

Ra Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,

Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weing A.H., Wang X.,

Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

"The genome sequence of Drosophila melanogaster.";

RI Tolobs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Princelle R.G., Marker B.G., Marker B.G., Marker B.G., Andrews-Pfannkoch C., Baldwin D., Princelle R.G., Pri
                                                                                Query Match
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished observations (SEP-2000).

-i- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way use by non-profit institutions as its content is in no way the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003609; AAF52225.1; ALT_SEQ. FlyBase; FBgn0031688; Cyp28d2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                         Endoplasmic reticulum; Hypothetical protein
BINDING 446 446 HEME (BY SIMILARITY)
                                                                                                                                                                                                                                                                                               Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
                                                                                                                                                                              SEQUENCE
                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidized flavoprotein + H(2)0.
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: Ref. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001128; Cytochrome_P450
                                                                                                                                                                                   501 AA;
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence differs from that shown due to erroneous
                                                                                                                                                                                            58222 MW;
                                                             20.8%;
                                                                                                   16.5%;
                  11;
                                                   Score 61.5;
Pred. No. 4.
                                                                                                                                                                                            9AD85F249390A655 CRC64;
                  Mismatches
                                                                                                            DB 1;
                       34; Indels 35; Gaps
                                                                                                            Length 501;
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SGAH_ECOLI
ID SGAH_I
AC P3930
                                                                                                                            망
                             Query Match
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGAH_ECOLI
P39304;
               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
probable hexulose-6-phosphate parabhase (EC 4.1.2.-) (HUMPS) (D-arabino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
"Novel phosphotransferases system genes revealed by bacterial genome analysis: operons encoding homologues of sugar-specific permease domains of the phosphotransferase system and pentose catabolic enzymes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGAH OR B4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95334362; PubMed=7610040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 YPVSQSVCKKFVEYIRRQQQMATSEGLDAMDLSLCYTTEVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region from 92.8 through 100 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Analysis of the Escherichia coli genome VI: DNA sequence of the
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 YYRNADICSR-----HRVTSAGLTLQDLQLWCNLRII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 HKTYATDFRSF-HNNEWRNFVNKKTDMILGNNPFVLTGDEWKERRSEIMPALSPNRVKAV 151
                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: CONDENSATION OF D-RIBULOSE 5-PHOSPHATE WITH FORMALDEHYDE TO FORM D-ARABINO-6-HEXULOSE 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 143:2519-2520(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Is the ribulose monophosphate pathway widely distributed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reizer J., Reizer A., Saier M.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97419490; PubMed=9274005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISCUSSION OF SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enome sci. Technol. 1:53-75(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HEAHKTSLSSWKHDQDWANVSN----MTFSNGKL-----
                                                                                              EcoGene; EG12496; sgaH.
InterPro; IPR001754; OMPdeca
Pfam; PF00215; OMPdecase; 1.
                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE HUMPS FAMILY
                                                               SEQUENCE
                                                                                                                                                 SWISS-2DPAGE; P39304; COLI.
                                                                                                                                                                                 EMBL; U14003; AAA97092.1; -.
                                                                                                                                                                                                                                                                                                                                                                  SGAU AND SGAE
                                                                                                                                                                   AE000491;
l Similarity
17; Conserv
                                                                                Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-phosphate formaldehyde lyase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MG1655;
                                                                    216 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                   AAC77153.1; -
                                                                    23578 MW;
                   16.0%;
23.6%;
                                                                                                                     OMPdecase.
     16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                     Score 59.5; DI Pred. No. 3.1;
                                                                      EC8490DA1D02D824 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AA
                                        DB 1; Length 216;
                                                                                                                                                                                                                                                       Usage
          Indels
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Matches
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Best Local
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                                                                                                                    Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin METAL 212 212 IRON (BY SIMILARITY).
                                                                                              SEQUENCE
                                                                                                           METAL
                                                                                                                                                PROSITE; PS00185; IPNS_1; 1. PROSITE; PS00186; IPNS_2; 1.
                                                                                                                                                                      PRINTS; PR00682; IPNSYNTHASE.
                                                                                                                                                                                InterPro; IPR002283; IPN_synth.
InterPro; IPR002057; Isopen_N_synth.
Pfam; PF03171; 20G-FeII_Oxy; 1.
                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                    EMBL; M19421; AAA26770.1; -. EMBL; A01132; CAA00131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and nucleotide sequence determination of the isopenicillin N synthetase gene from Streptomyces clavuligerus.";

Gene 62:187-196(1988).

-I- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.

-I- COPACTOR: IRON AND ASCORBATE.
                                                                                                                                                                                                                 InterPro; IPR005123; 20G-FeII_Oxy.
                                                                                                                                                                                                                                         PIR; A29894; A29894.
                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND
                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE-88212175; PubMed-3130293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leskiw B.K., Aharonowitz Y., Mevarech M., Wolfe S., Vining L.C., Westlake D.W.S., Jensen S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Isopenicillin N synthetase (EC 1.-.-) (IPNS) (Isopenicillin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRCL
            1 HEAHKTSLSSWKHD------ODWANVSNMTFS--NGKLRVKGIYYRNADICSRHRVTSA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P10621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 LEDLPLFKGIPI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 TGYWTWEQAQQWRDAGIGQVVYHRSRDAQAAGVAWGEADITAIKRLSDMGFKVTVTGGLA 173
                                                                                                                                                                                                                                                                                                                                                                                CEPHALOSPORIN.
SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                  P05326; 1BLZ
                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSLSSWKHDQDW--ANVSNMTFSNGK-LRVKGIYYRNADICSRHRVT-----SAGLT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQDLQLWCNLRI 66
                                                         Similarity
                                                                                           329 AA;
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                         268 I
36958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomycineae; Streptomycetaceae; Streptomyces
                                                        25.7%;
                                                                  16.0%;
                                       10; Mismatches
                                                     Score 59.5;
                                                     Pred.
                                                                                               IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                   71AA1CCE9514761C CRC64;
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                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                                                              DB 1;
                                         33;
                                                                                                                                                                                                                                                                                                         Usage
                                                             Length 329;
                                        Indels
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                                       9
                                    Gaps
                                    2
RESULT 9
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                                                                                                                                                                                                                                                                                                             IL1B_TRIVU
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RESULT 8
Y108_CHLTR
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                                             Trichosurus vulpecula (Brush-tailed possum)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Diprotodontia; Phalangeridae;
                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
NCBI_TaxID=9337;
                                                                                         Interleukin-1 beta precursor (IL-1 beta)
                                                                                                                                                                                         Q9XS77
                                                                                                                                                                                                        IL1B_TRIVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 251 AA; 27474 MW; A4C2F6BE7517298E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHCI-2DPAGE; O84110; -- InterPro; IPR002678; DUF34. Pfam; PF01784; DUF34; T
                                                                                                                                                                                                                                                                                                        162 ALGGKKRVSSAAL 174
                                                                                                                                                                                                                                                                                                                                                                        102 DAHTTIGNNWKVARDLGWEQLESFGSSQPSLGVKGVFPEMEVHDFISQLSAYYQTPVLAK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIGRFAMS; TIGR00486; DUF34; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001284; AAC67699.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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O84110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 282:754-759(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., An Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99000809; PubMed=9784136;
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16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                44 ---SRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein CT108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                               2 EAHKTSLSSWK--HDQDWANVSNMTFSNGKLRVKGI------YZRNADIC- 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GTPMHEVNLW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 GLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDHPMIAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.7%;
26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.5; DB
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                             269 AA.
                                                                                                               update)
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  Trichosurus.
                        Euteleostomi;
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RESULT 10
YRAN_HAEIN
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Medlock D.N., Goh L.P., Parlane N.A., Buddle B.M.;
Medlock T. Goh L.P., Buddle B.M.;
Medloc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
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pfam; pF02394; IL1_propep; 1.
prINTS; pR00252; IL1HBGF.
proDom; pp002526; Interleukin_1; 1.
SMART; SM00125; IL1; 1.
pR0SITE; pS00253; INTERLEUKIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002348; IL1_HBGF.
InterPro; IPR003502; IL1_propep.
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF071539; AAD21871.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine; Macrophage; Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                              p45300;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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SUBJUNIT: MONOMER.

DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSOR SEQUENTINE FUNCTION. AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. AMINO ENDS OF THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SEGMENTS DATASET OF THE PROCURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETED BY DAMAGED COLLABOR.
                                                                                                                                                                                                        Hypothetical protein HI1656.
                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                        Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                          YRAN_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 DSSFRLVSSQDCTIQDINQKCLALSKASELRALH 150
NCBI_TaxID=727;
                                                                Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 HQFHQTVMVIVAIEKMKHLNGLSSQFFQDNDLMNIFTNIFQE----EPITFKNCDIYES 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 -CSRHRVTSAGLTLQDLQLWC-----NLRIIH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HEAHKT-----SLSSWKH------DQDWANVSNWTFSNGKLRVKGIYYRNADI--- 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECRETORY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%;
24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58.5; Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
INTERLEUKIN-1 BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inflammatory response; Pyrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307A1FE3B627D6E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Rd / KW20 / AGCC 51907;

MEDLINE=95350630; PubMed=7542800;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Islands C.A., Gocayne J.D.,

McKenney K., Sutton G., Fitchugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek B., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no no many of the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.accommendation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG, TO E.COLI YRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32838; AAC23300.1; -. TIGR; HI1656; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 119 AA; 13812 MW; B7359D8181F31AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0252; TIGRO0252; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02021; UPF0102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hemorrhagic protein-inodostomin precursor (EC 3.4.24.-) (RHO)
                                                                                                                                                                                                                                                                                      Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P30403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISR_AGKRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 Q-W 113
                                                                                                                                                      TISSUE=Venom gland;
MEDLINE=93277962; PubMed=7916635;
                                                                         precursor of platelet aggregation inhibitor and hemorrhagic protein from Calloselasma rhodostoma venom.";
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=8717
                                                                                                                                                                                                                                                       Viperidae; Crotalinae; Calloselasma.
                                                                                                                                                                                                                                                                      Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                     Contains: Disintegrin rhodostomin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 HSAYGSAIESVDWRKOOKWLDAANLWLAKONMSLE-----DANCREDLIAFGKTPODI 111
    TISSUE=Venom gland
                  SEQUENCE OF 77-478 FROM N.A.
                                                            Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 QLW 61
                                                                                                               Nucleotide sequence of a full-length cDNA encoding a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HEAHKTSLSS--WKHDODWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLODL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003509;
                                                          Biophys. Acta 1173:243-245(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.5%; Score 58; DB 1; Length 119; 23.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UPF0102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pfam; pF00200; disintegrin; 1.
Pfam; pF01421; Reprolysin; 1.
Pfam; pF01421; Reprolysin; 1.
Pfam; pF01562; Pep_M12B_propep; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOM; PR000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS500121; ADAM_MEPRO; 1.
PROSITE; PS500127; DISINTEGRIN_1; 1.
PROSITE; PS001427; DISINTEGRIN_2; 1.
PROSITE; PS001427; ZINC_PROTEASE; 1.
PROSITE; PS001427; ZINC_PROTEASE; 1.
            DISULFID
                           METAL
                                                                        METAL
                                            METAL
                                                                                         PROPEP
                                                          ACT_SITE
                                                                                                        CHAIN
                                                                                                                        PROPEP
                                                                                                                                                                Hydrolase; Metalloprotease; Zinc; Blood coagulation; Platelet; Cell adhesion; Venom; Zymogen; Glycoprotein; Signal.
                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR00133; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L08780; AAA49196.1; -. PIR; J01301; J01301
PIR; S3792; S33792.
HSSP; P17494; 1KST.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M12.161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: INHIBITS FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. ACT BY BINDING TO THE GLYCOPROTEIN IIB-IIIA RECEPTOR ON THE PLATELET SURPACE AND INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Disintegrins: a family of integrin inhibitory proteins from viper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91046142; PubMed=2236100;
Gould R.J., Polokoff M.A., Friedman P.A., Huang T.-F., Holt J.C.,
Cook J.J., Niceviarowski S.;
"Disinterial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91046142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 408-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Au L.-C., Huang Y.-B., Huang T.-F., Teh G.-W., Lin H.-H., Choo K.-B. Acommon precursor for a putative hemorrhagic protein and rhodostomin, a platelet aggregation inhibitor of the venom of calloselasma rhodostoma: molecular cloning and sequence analysis."; Biochem. Biophys. Res. Commun. 181:585-593(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93135775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92095959; PubMed=1755841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Thodostomin, an RGD-containing peptide expressed from a synthetic
gene in Escherichia coli, facilitates the attachment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 408-475 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: BINDS ONE ZINC ION.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGREGATION INDUCED BY ADP, THROMBIN, PLATELET-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTS IN HEMORRHAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H.H., Hu S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys. Res. Commun. 190:242-249(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exp. Biol. Med. 195:168-171(1990).
ON: THIS PROTEIN IS A ZINC PROTEASE FROM SNAKE VENOM THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7916592;
 ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
                                                                                            RHODOSTOMIN
                                                                                                                        HEMORRHAGIC PROTEIN
                                                                                                                                                            POTENTIAL.
SIMILARITY
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                                                                                           MEDLINE=95084159; PubMed=7992054; Minvielle-Sebastia L., Preker p.T., Keller W.; "RNA14 and RNA15 proteins as components of a yeast pre-mRNA 3'-end processing factor."; Science 266:1702-1705(1994).

-!- FUNCTION: COMPONENT OF THE CLEAVAGE FACTOR I (CF I) INVOLVED IN PRE-MRNA 3'-END PROCESSING. INTERACTS WITH FIP1 AND PROCEABLY AI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                            -1- SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC-1- SIMILARITY: CONTAINS 6 HAT REPEATS.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-S288c / AB972;
Devlin K., Churcher C.M.,
                                                                                                                                                                                                                           Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                  FUNCTION
                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 28583 / FL100;
                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                               mRNA decay rate; sequence analysis reveals an RNA-binding domain the RNA15 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                        Minvielle-Sebastia L., Winsor B., Bonneaud N., Lacroute F., "Mutations in the yeast RNA14 and RNA15 genes result in an a
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 28583 / EL100;
MEDLINE-91246175; PubMed-1674817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RN14_YEAST
P25298;
                                                                                                                                                                                                                                                                                                                                                       REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
mRNA 3'-end processing protein RNA14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INKNA 3'-end processing protein RNA14.
RNA14 OR YMR061W OR YM9796.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 YKYMHFGISLVNLETWCNGDLIN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 TNWESDEPIKKYSQLNLNHEIKRHYDIVVYVDSRFCTKHSNDLEVIRKFVHEVVNAIIES 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 -----GLTLQDLQLWCNLRIIH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 SSWKHDQDWANVSNMTFSNG-KLRVKGIYYRNADICSR----
                                                                                                                                                                                                                                                                                            (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                      Biol. 11:3075-3087(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%;
20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54006 MW;
                                                                                                                                                                                                                                      Barrell B.G., Rajandream M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL ATTACHMENT SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6490A2B171D3A830 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HRVTSA----
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                                                                                               PROBABLY ALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                     "A nonsense mutation in a novel gene is associated with pigmentosa in a family linked to the RP1 locus."; Hum. Mol. Genet. 8:1541-1546(1999).
-i- FUNCTION: COULD HAVE A ROLE IN THE DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                   Pierce E.A., Quinn T., Meehan T., McGee T.L., Berson "Mutations in a gene encoding a new oxygen-regulated protein cause dominant retinitis pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sullivan L.S., Heckenlively J.R., Bowne S.J., Zuo J., Hide W.A., Gal A., Denton M., Inglehearn C.F., Blanton S.H., Daiger S.P., "Mutations in a novel retina-specific gene cause autosomal dominant retinitis pigmentosa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Oxygen-regulated protein 1 (Retinitis pigmentosa
                                                                                                                                                                                  Guillonneau X., Piriev N.I. Jacobson S.G., Farber D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RP1_HUMAN
P56715;
                                                                                                                                                                                                                               MEDLINE=99330563; PubMed=10401003;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99318095; PubMed=10391211;
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99318096; PubMed-10391212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Retinitis pigmentosa 1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 QEWLNV-----TNGLKRASPINLRTANKKNIPQPGTSDSNIQQLQIWLN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 QDWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWCN 63
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PEAT 56 88 HAT 1.
PEAT 90 124 HAT 3.
PEAT 138 170 HAT 3.
PEAT 181 214 HAT 4.
PEAT 257 289 HAT 6.
PEAT 298 330 HAT 6.
DUENCE 677 AA; 79960 MW; 1024
                                               PHOTORECEPTOR CELLS.
TISSUE SPECIFICITY: EXPRESSED IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR ORP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet.
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A40257; A40257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0004665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00386; HAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003107;
                                                                                                                                                                                                                                                                                                     22:248-254(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22:255-259(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA14.
                                                                                                                                                                                                     Piriev N.I., Danciger M., Kozak C.A., Cideciyan A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 H
124 H
170 H
214 H
289 H
330 H
79960 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57.5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102433295FE7CD63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e 57.5;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat.
N RETINA. NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2156 AA
                                                                                                                                                             associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RP1 protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THR-1670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                           E.L., Dryja T
photoreceptor
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                                                                                            OF,
                                                                                                                                                               retinitis
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                                                                                                                                                                                                                                                                                                                                                                     T.P.;
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PLACENTA,

LUNG,

LIVER,

SKELETAL

NOT EXPRESSED

KIDNEY,

SPLEEN AND IN HEART

Baras

1_MOUSE FCG1_MOUSE FCG1=MOUSE P26151; 01-MAY-1992 01-MAY-1992 15-JUN-2002

STANDARD;

PRT;

404

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High affinity immunoglobulin gamma

(Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41) for the control of the control

RESULT

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B
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                                                                                                                              Matches
                                                            Query Match
Best Local
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EMBL; AF143225; AAD44197.1; J
EMBL; AF143225; AAD44198.1; -
EMBL; AF143221; AAD42072.1; -
EMBL; AF141021; AAD46774.1; -
EMBL; AF152242; AAD46774.1; J
EMBL; AF152240; AAD46774.1; J
EMBL; AF152240; AAD46774.1; J
EMBL; AF146592; AAD46769.1; -
                                                                                                                                                                                                                                                                                                    InterPro; IPR003533; DC Pfam; PF03607; DCX; 2. SMART; SM00537; DCX; 2.
                                                                                             SEQUENCE
                                                                                                                    VARIANT
                                                                                                                                         VARIANT
                                                                                                                                                                VARIANT
                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
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  666
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                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                  Vision;
                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                        MIM; 180100;
                                                                                                                                                                                                                                                                                                                                                                  Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use
                                                           Local
                     6 TSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PANCREAS.

DISEASE: DEFECTS IN RP1 CAUSE RETINITIS PIGMENTOSA FORM 1 (RP1); IDISEASE CHARACTERIZED BY CONSTRICTION OF THE VISUAL FIELDS, NIGHT BLINDNESS, AND FUNDUS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED WITH TRUNCATED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WWW-"http://www.sph.uth.tmc.edu/retnet/".
DATABASE: NAME-Mutations of the RP1 gene;
NOTE-Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://www.retina-international.com/sci-news/rp1mut.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE: NAME=RetNet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS
SSVASKKKKKSRQQAINSRYQDGQLATKGILNKNERINTKGRITKE-MIVQD
                                                                                                                                                                                                                                                                                                                                                    603937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE-Retinal information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF143226; AAD44197.1;
                                               l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                               HGNC:10263; RP1.
                                                                                                                                                                                                                                                                                 Retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                             PS50309;
                                                                                                                                         1691
                                                                                                                                                                1670
                                                                                           2156 AA;
                                                                                                                    2033
                                                                                                                                                                                                            36
154
268
671
1687
872
                                               Conservative
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                                                                                                                                                                                                           pigmentosa;
118 D
233 D
273 P
675 P
1691 P
872 R
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                                                                                                                  2033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  license agreement (See http://www.isb-sib.ch/announce/
                                                        15.4%;
                                                                                           240659 MW;
                                             13;
                                                                                                                                                                                                                                                                                                                                                                                    JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOINED
                                                        Score 57.5;
Pred. No. 81;
                                                                                                                 /FTId=VAR_007813
C -> Y
                                                                                                                                                                                     /FTId=VAR_007810
N -> Y
                                                                                                                                         Ś
                                                                                          /FTId=VAR_007814.
W; 55AEDBEC43D6A507 CRC64;
                                                                                                                                                                                                                       POLY-SER.
                                                                                                                                                                                                                                  POLY-LYS.
                                                                                                                                                                                                                                              POLY-SER.
                                                                                                                                                                                                                                                           DOUBLECORTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 network;
                                                                                                                                                   /FTId-VAR_007812
                                                                                                                                                                                                                                                                     DOUBLECORTIN
                                                                                                                                                                         /FTId=VAR_007811
                                                                                                                                                                                                                                                                              Polymorphism; Repeat.
                                                                                                                                                                                                             ť
                                             Mismatches
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MEDILINE-92166399; PubMed=1531670;

Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;

Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;

"Structure and mapping of the gene encoding mouse high affinity gamma RI and chromosomal location of the human Fc gamma RI gene.

J. Immunol. 148:1570-1575(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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PIR; A46480; A46480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: MACROPHAGE SPECIFIC.
-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-i- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor
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SMART; SM00408; IGC2; 1.
IgG-binding_protein; Receptor;
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:95498; Fcgrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M31314; AAA40056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.; "Molecular cloning and expression of the mouse high affinity Fc receptor for IqG.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                       [mmunoglobulin
17 WAN--VSNMTF-SNGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. HIGH AFFILITY RECEPTOR.
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                            Similarity 22; Conserv
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IG-LIKE C2-TYPE DOMAIN 1.
                                         Score 56.5;
Pred. No. 15;
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1C4F0033842767E7 CRC64;
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                                                                                                                                                                                                                                                                                                                            "Shimizu H., Saitoh Y., Suda Y., Uehara K., Sampei G.,
"Complete nuclectide sequence of the F plasmid: its in
organization and diversification of plasmid genomes."
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
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Shimizu H., Saitoh Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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m SWISS\text{-}PROT} entry is copyright. It is produced through a collaboration een the {
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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373
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Result	Score	Query Match 1	Length	BB	ID	Description
1	67	18.0	296	2	E72203	
N	67	18.0	307	N	T46103	hypothetical prote
ω	٠.	17.3	276	N	E96990	
4	63.5	17.0	263	μ	S31323	orotidine-5'-phosp
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11	59.5		216	N	D91275	
12	9		216	N	D86116	probable hexulose-
13	9		329	2	A29894	
14	φ		427	N	F83984	1
15	59		187	N	T15023	hypothetical prote
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17	58.5	15.7	251	N	C71557	, W
18	58		119	N	C64174	hypothetical prote
19	58		330	Ν	C71096	
20	58		646	2	T02643	1 prot
21	7		478	ν	JQ1301	hagic prot
22	57.5		677	N	S54561	
23	7	15.4	729	N	A97747	FΛ
24	7	•	1063	N	S18211	hypothetical prote
25	57		345	N	D97407	hypothetical prote
26	57	15.3	345	N	AE2625	conserved hypothet
27	57	•	398	N	AC1998	hypothetical prote
28	σ	•	216	N	10	probable hexulose-
29	56.5	15.1	280	N	155577	Fc gamma (IgG) rec

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4444033333334 4444033354 54431

ALIGNMENTS

conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

Hic

C; Accession: E72203 R; Nelson, K.E.; Clay

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hypothetical protein T25B15.100 - Arabidopsis thaliana (). Species: Arabidopsis thaliana (mouse-ear cress) (). Species: Arabidopsis thaliana (mouse-ear cress) (). Species: Arabidopsis thaliana (mouse-ear cress) (). C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 (). Arcession: T46103 (). Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000 A;Reference number: Z23021 A;Accession: T46103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: TM1852
A;Gene: TM1852
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1107
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A;Accession: E72203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-296 <ARN>
A;Cross-references: GB:AE001822; GB:AE000512; NID:g4982429; PIDN:AAD36914.1; PID:g498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-307 <ALC>
A;Cross references: EMBL:AL132972
A;Experimental source: cultivar Columbia; BAC clone T25B15
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                                                       A; Map position: 3
A; Introns: 63/3; 2:
A; Note: T25B15.100
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Query Match
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llarity 27.3%; Pred. No. 2.2;
Conservative 11; Mismatches
                                                                                      225/2; 267/3
      18.0%;
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      Length 307;
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probable siderophore receptor PA1365 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
                                                                         RESULT 5
F83476
                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Merckelbach, A.; Goedecke, S.; Janowicz, Z.A.; Hollenberg, C.P. submitted to the EMBL Data Library, November 1992
A;Description: Cloning and sequencing of the URA3 locus of the methylotrophic yeast Hans A;Reference number: S31323
A;Accession: S31323
                                                                                                                                                           밁
                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:x69461; NID:g2783; PIDN:CAA49221.1; PID:g2784
C;Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase
F;3-263/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-263 <M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Pichia angusta
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000 C;Accession: S31323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (Pichia angusta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee ; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CAC0736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: GB:AE001437; PIDN:AAK78712.1; PID:q15023617; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-276 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E96990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 NWK-DESWIDVSNIKWDNYVVNTIGKNIKNKGVDGFFIDNIDVYSKYKKDSMFIGLINI 162
                                                                                                                                                         90
                                                                                                                                                                                      14 DQDWANVSNMTFSNGKLRVKGIYYRN---ADICSRHRVTSAGL 53
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SWKHDQDWANVSNMTFSN-----GK-LRVKGI---YYRNADICSRHRVTSAGLTLQDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HEAHKTSLSSWKHDQDW------
                                                                                                                                                  DRKFADIGNTV----KLQYKGGIYRTSKWADITNAHGVTGAGI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWTDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HDEYKVLSFIWRHNKEWKVRSEHHVLVLGARTSWKKTQCHIHHLPYSQG-ITINGVLYYG 207
                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                1-263 <MER>
                                                                                                                                                                                                                                       Conservative
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39.5%;
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                                                                                                                                                                                                                                                       Score 63.5; D
Pred. No. 5.1;
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Pred. No. 4.
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9; Mismatches
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                                                                                                                                                                                                                                                                             DB 1; Length 263;
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               A; Experimental source: clone Y70C5D C; Genetics:
                                                                                                                                     A; Reference number: 220352
A; Accession: T27354
                                                                                                                                                                                                        R;Steward,
                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone T25E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z20009
A; Accession: T25282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Matthews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: z19339
A; Accession: T20881
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A; Residues: 1-813 <STO>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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A; Molecule type: DNA
A; Residues: 1-1101 <WI4>
A; Cross-references: EMBL; ALO21507; PIDN: CAA16430.1; GSPDB: GN00023; CESP: T25E12.4a
                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1101 <WI3>
A;Cross-references: EMBL:AL021572; PIDN:CAA16519.1; GSPDB:GN00023; CESP:T25E12.4a
                                                                                                                                                                                                  submitted to the EMBL Data Library, January 1998
                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Restidues: 1-1101 <WIZ>
A;Cross-references: EMBL:Z82052; PIDN:CAB04830.1; GSPDB:GN00023; CESP:T25E12.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1996
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A;Residues: 1-1101 <WTL>
A;Cross-references: EMBL:Z92967; PIDN:CAB07478.1; GSPDB:GN00023; CESP:T25E12.4a
                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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28.8%; Pred. No. 19;
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Matches Query Match

DNA Res. 8,

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A;Introns: 13/3; 77/1; 98/2; 201/1; 263/3; 310/1; 398/3; 440/3; 469/3; 506/1; 541/1; 571 C;Superfamily: protein kinase C zinc-binding repeat homology F;322-371/Domain: protein kinase C zinc-binding repeat homology <KZN1>F;474-523/Domain: protein kinase C zinc-binding repeat homology <KZN2>
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al10476
C;Superfamily: Synechocystis hypothetical protein s1r2144
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A; Accession: AC1866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-274 <KUR>
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NA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycosyl hydrolase/lysozyme lyc [imported] - Agrobacterium tumefaciens (strain C58, Dupd C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Date: 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: AI2836 T.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, IR;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, IR;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellerage, G.; Gillet, G.; Guenthner, G.; Guenth
                                                                                                                                                                                                                                                                                                            A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193
A;Accession: AI2836
A;Status: preliminary
A;Status: preliminary
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: lyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                            A;Cross-references: GB:AE008688; PIDN:AAL43111.1; PID:g17740583; GSPDB:GN00186
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 992 WKEISENATEFINGLLOVK------MSKRYTVTKAQSQIWMQNYTLWSDLRVL 1038
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es 17; Conserv
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A; Residues: 1-354 <KUR>
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                                                                                                                                                                                   C; Superfamily: hypercare; carbon-carbon lyase C; Keywords: aldehyde-lyase; carbon-carbon lyase
                                                                                                                                                                                                                                                                               A; Gene:
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Query Match

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A; Map position: circular chromosome
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Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable hexulose-6-phosphate synthase (EC 4.1.2.-) [similarity] - Escherichia coli (N. Alternate names: hypothetical protein o216
                                                                                                                                                                                             A; Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97092.1; PID:g537037
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Recession: G65230
A; Accession: G65230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                           A;Cross-references: GB:AE000491; GB:U00096; NID:g2367357; PIDN:AAC77153.1; PID:g17906
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-216 <BLAT>
                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown
Superfamily: hypothetical protein HI1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HEAHKTSLSSWKHDQDWANV--SNMTF----SNGKLRVK---GIYYRNA 40
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Pred. No.
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                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-216 <STO>
                                                                                                                                                                                                                                                                                             A;Status:
                                                                                                                                                                                                                                                                                                           A; Accession: D86116
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                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     probable hexulose-6-phosphate synthase sgaH [imported] - Escherichia coli (strain O157:HC;Species: Escherichia coli
                                                                               Query Match
Best Local Similarity 23.68; Score 59.5;
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                                                                                                                                                                                                                                                                                               Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 Reference number: A85480; MUID:21074935; PMID:11206551
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A; Residues: 1-216 <HAY>
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    6 TSLSSWKHDQDW--ANVSNMTFSNGK-LRVKGTYYRNADICSRHRVT-----SAGLT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 TGYWTWEQAQQWRDAGIQQVVYHRSRDAQAAGVAWGEADITAIKRLSDMGFKVTVTGGLA 173
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Similarity 23.6%; Pred. No. 12;
17; Conservative 16; Mismatches
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23.6%; Pred. No. 12;
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                                              28; Indels 11; Gaps
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RESULT 15
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A:Gene: BH2678
C:Superfamily: succinyl-diaminopimelate desuccinylase
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                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-427 <STO>
                                                                                                                                                                                                                                                                                                                                                            R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masul, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Leskiw, B.K.; Aharonowitz, Y.; Mevarech, M.; Wolfe, S.; Vining, L.C.; Westlake, D.W Gene 62, 187-196, 1988
A;Title: Cloning and nucleotide sequence determination of the isopenicillin N synthet
A;Reference number: A29894; MUID:88212175; PMID:3130293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-329 <LES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces clavuligerus C;Species: Streptomyces clavuligerus C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-May-2000
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419 YEWCHLR 425
                                               361 EEVKTSMSQTVTDGGWLAEAGIPTLLFGPGKLEDAHSVNEELEIAELVQYTKTLLTF--I 418
                                         59 QLWCNLR 65
                                                                                  2 EAHKTSLSSWKHDQDW----ANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDL 58
                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HEAHKTSLSSWKHD------ODWANVSNMTFS--NGKLRVKGIYYRNADICSRHRVTSA 51
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                                                                                                    16.0%; Suc. No. 29.9%; Pred. No. 2. 1. Mismatches
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T15023
hypothetical protein Y1108 - Yersinia pestis plasmid pMT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C;Accession: T15023; T14697
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T15023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF074611; NID:g3883003; PID:g3883106; PIDN:AAC82766.1 R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano, submitted to the EMBL Data Library, March 1998 A;Description: Structural organization of virulence determinants in three Yersinia pesti A;Reference number: 218168 A;Accession: T14697
                                                                                                                                                                                                                                                                                                                                                            A;Gene: Y1108
A;Genome: plasmid pMT1
C;Superfamily: Yersinia pestis plasmid pMT1 hypothetical protein Y1108
Search completed: December 8, 2002, 19:34:47 Job time: 26.8129 secs
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A;Molecule type: DNA
A;Residues: 1-187 <HUP>
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A; Residues: 1-187 <LIN>
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Best Local Similarity
Matches 13; Conserv
                                                                                                                         124 DWADVANWLEANGRLK-----ENAELAHNARVLS 152
                                                                                                                                                            16 DWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTS 50 | | | | : | : | | : | | | | |
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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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59.55
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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US-08-995-659-13
US-09-215-649A-13
US-09-957-780-13
US-08-996-139-11
US-08-996-139-11
US-08-996-139-11
US-08-996-139-11
US-08-996-139-11
US-08-942-842-7
US-08-98-362-2
US-09-052-521C-34
US-08-994-031-100
US-08-94-031-100
US-08-94-031-100
US-08-94-031-102
US-09-413-231-5
US-09-413-231-5
US-08-136-138-1
US-08-711-430-2
US-08-711-430-2
US-08-761-136-1
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     PCT-US93-11703-75
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138.199 Million cell updates/sec
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11, Appl
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100, App
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US-08-637-323-1 US-07-940-605A-3 US-07-940-605A-3 US-07-940-605A-2 US-08-184-422-8 US-08-184-422-4 US-08-446-922-4 US-08-446-922-4 US-08-446-922-4 US-08-490-96-2 US-08-49-199-12 US-08-497-7338-12 US-08-771B-8 US-08-771B-8 US-08-783-915-12 US-08-783-915-12 US-08-783-915-12 US-08-783-915-12 US-08-783-915-12 US-08-783-913A-12
Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 12, Appli

RESULT 1

ALIGNMENTS

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Sequence 13, Application US/08996139

Patent No. 6017729

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Maraskovsky, Eugene
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
US-08-996-139-13
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: USSN 60/06
APPLICATION NUMBER: 1997
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/81
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                        INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
CURRENT APPLICATION DATA:
                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430 TELEFAX: (206)233-0644
                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 51 Uni
CITY: Seattle
STATE: WA
                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                NAME:
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                                                                                                                                                                                                                  Perkins, Patricia Anne RATION NUMBER: 34,693
                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                UMBER: USSN 08/813,509
07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 DECEMBER 1997
                    protein
                                                                                                                                                                                                                                                                                                                                                                                                               USSN 60/064,671
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US-09-215-649A-13
                       RESULT 3
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                                                                                                                  Matches
                                                                                                                                           Query Match
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US-08-995-659-13
/ Sequence 13, Application US/08995659
Patent No. 6242213
Patent No. 6242213
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                                                                                                                                                                                                                                             TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
                                         179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                       CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                        Local Similarity 60.0 es 36; Conservative
                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 22 DEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 51 Uni
CITY: Seattle
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                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                           : (206)587-0430
(206)233-0644
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                                                                                                                                                                                             linear
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Maraskovsky, Eugene
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14 OCTOBER 1997
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                                                                                                                        47.7%;
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60.08;
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                                                                                                      5; Mismatches
                                                                                                Score 178; DB 4; Length 317; Pred. No. 2.6e-15; Indels 5; Mismatches 17; Indels
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Pred. No. 2.6e-15;
5; Mismatches 17; Indels
                                                                                             Gaps
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FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                  RESULT 4
US-09-052-521C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13
                                                                                                                                                                                    Sequence 4, Application US/09052521C Patent No. 6316408 GENERAL INFORMATION: BOYLE, William J.
                                                                                                                                           TITLE OF INVENTION: Ostec
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6271349
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/996,139
FILING DATE: CUnknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
FILING DATE: 23 DECEMBER 1996
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                               Match 47.7%;
Local Similarity 60.0%;
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M. Galibert, Laurent
PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                     Osteoprotegerin Binding Proteins and Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 178; DB 4;
Pred. No. 2.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 317;
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US-09-052-521C-4
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TYPE: PRT
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                                                                  Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
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                                                                                                                                                                                                                                                                                                                             FILING DATE: 4Unknown Application Number: USSN 08/813,509 Application Number: USSN 08/813,509 Application Number: USSN 08/813,509 Application Number: USSN 08/772,330 Application Number: 23 December 1996 Filing Date: 23 December 1996 ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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                                                                                    Local
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                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 2852-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                    36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                   LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                  TELEPHONE: (206)587-0430
                                                                    Conservative
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                                                                                       47.78;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <Unknown>
                                                                         5; Mismatches
                                                                                       Score 178; DB 4;
pred. No. 2.6e-15;
                                                                                                           DB 4; Length 317;
                                                                                Indels
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RESULT 6

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us-08-996-139-11
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                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-996-139-11
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                                                                                                                                                                       ; Sequence 11, patent No. 6
                                                                                                                                                                                                                  US-08-995-659-11
                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 1
FILING DATE: 07 MARCI
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23 DECEMBER 1990
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatif
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                                                                    APPLICANT: Anderson, Dirk M.
APPLICANT: Gallbert, Laurent
APPLICANT: Maraskovsky, Eugene
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                    156 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 215
                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                       3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
CITY:
                 STREET:
                     ADDRESSEE: Inhidies Corporate STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                              34; Conservative
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                                                                                                                                                                               1, Application US/08995659 6242213
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amino acid
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   Seattle
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                                     Immunex Corporation, Law Department
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                                                                                                                                                                                                                                                                                                                                                                46.1%; Score 172; DB 3; Length 294;
56.7%; Pred. No. 1.5e-14;
ative 6; Mismatches 18; Indels
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COUNTRY:

USA

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US-09-215-649A-11
Sequence 11, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-995-659-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 SHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGEYYLYANICERHHETSGSVPTDYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating

COFFINATION OF THE STATEM OF THE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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                 APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: WA
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Microsoft Word for Power Macintosh 6.0.1
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56.78;
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US-09-577-780-11
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GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 11:
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                                         APPLICATION NUMBER: 08/995,659
FILING DATE: <UGKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTMARE: Microsoft Word for Power Macintosh 6.0.1
SOFTMARE: MICROSOFT WORD FOR APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILLING DATE: 24-May-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappab
NUMBER OF SEQUENCES: 19
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 197
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            TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
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RESULT 10
US-08-842-842-7
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Patent NO. 5843678
GENERAL INFORMATION:
APPLICANT: BOYLE, William J.
APPLICANT INVENTION: OSTEOPROTEGE
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARATERISTICS:
LENGTH: 316 amino accorded to the control of the con
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US-08-989-362-2
                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                             APPLICANT: Morman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
TITLE OF INVENTION: Reagents
VINUABER OF SEQUENCES: 2
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 SHKYTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               watch 46.1%; Score 172; DB 2; Length 316; Local Similarity 56.7%; Pred. No. 1.6e-14; Local Similarity 6; Mismatches 18; Indels 18; Active 6; Mismatches 18; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYRRNADICSRHRVTSAGLTLQDLQL 60
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amgen Inc.
     DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.18; 56.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/842,842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A-451
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, MOLECULE TYPE: protein US-08-989-362-2
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US-09-052-521C-2
                                                                                                                             ; TYPE: PRT
; ORGANISM: Mouse
US-09-052-521C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
 В
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09052521C Patent No. 6316408
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                                                                                                                                                                            SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                      FILE REFERENCE: A-451BIV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-06-23
                                                          Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOYLE, William J. TITLE OF INVENTION: Osteopro
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,846

ETITING DATE: 13-DEC-1996
                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/8
PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 901 California Avenue
CITY: Palo Alto
STREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
| 178 | SHKVTLSSWYHDRGWAKISNMTLSNGKLKVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                           y Match
Local Similarity 56.7%;
                             3 AHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLODLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304-1104
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amino acid
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                            Osteoprotegerin Binding Proteins and Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.1%; Score 172; DB 4;
56.7%; Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/989,362
                                                                                                                                                                                                                                                                    08/842,842
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                                                                         6; Mismatches
                                                                                        Score 172; DB 4; Length 316; Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 316;
                                                                                18; Indels
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                                                                                        Gaps
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RESULT 13

US-09-052-521C-34

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US-08-594-031-100
                                                              INFORMATION FOR SEQ ID NO: 100:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5783182
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Bindin
FILE REFERENCE: A-451BrV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
COURSELING DATE: 1998-03-30
                                                  SEQUENCE CHARACTERISTICS
                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 34
                                                                                                                                                                                       FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR TOATTON NUMBER: 60/006,838
                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/09052521C Patent No. 6316408
                                   LENGTH:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THOMPSON, TIMOTHY C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
                                                                                                                                          NAME: Remenick, James
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 57.9%; Score 72; DB 4; Length 28;
hes 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 SHKVTLSSWYHDRGWAKIS 27
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                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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                                376 amino acids
                                                                                                  202-639-789(
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: BAKER & BOTTS, L.L.P.
1299 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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SYSTEM: DOS
     single
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                                                                                                                                                        36,902
                                                                                                                                         0A146-0110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/842,842
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US-08-594-031-102
    Query Match
16.9%; Score 63; DB 1; Length 376;
Best Local Similarity 22.1%; Pred. No. 3.1;
Matches 17; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-594-031-102
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                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
US-08-594-031-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 102, Application US/08594031 Patent No. 5783182
                                                                                                                     MOLECULE TYPE: PE
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                              ORIGINAL SOURCE:
                                                                                                               FRAGMENT TYPE:
                                                                                                                                                                                                                                                                            NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-339-7700
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/00
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                   TELEPHONE: 202 - 639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THOMPSON, TIMOTHY C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11near
MOLECULE TYPE: pep
                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08 FILING DATE: 30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20004-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 YGHATTVGVNMTDVMVW 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 HDSHNYSTNYKWSGDNTGVSTNHTVNHTYVNGTSNTVKAAAGCRSKTSGAGDNSRDNCNR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 H-RVTSAGLTLQDLQLW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HEAHKTSLS-SWKHDQDWANVS---NMTFSNG-----KLRVKGIYYRNADICSR 45
                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                                                                      376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: BAKER & BOTTS, L.L.P.
1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                      N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 16; Mismatches
                                                                                                                                                   peptide
                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.9%; Score 63; DB 22.1%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                              60/006,838
                                                                                                                                                                                                                                                                                                       0A146-0110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 376;
Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
 4;
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Page 7

DЬ

멍 46 H-RVTSAGLTLQDLQLW 61 : |: |: : |: :| 249 YGHATTVGVNWTDVMVW 265

Search completed: December 8, 2002, 19:35:33 Job time : 16.4774 secs

7		

OM protein - protein search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

Run on:

Title:

US-09-880-457-4

Scoring table: sequence: perfect score:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:*

sp_bacteria:* sp_archea:* sp_human:* sp_fungi:*

sp_invertebrate:*
sp_mammal:*

sp_organelle:* sp_phage:* sp_mhc:*

sp_plant:*

sp_rodent:*

Result

Score

Match Length DB

IJ

SUMMARIES

Q9DDZ5 Q88282

Q97BJ7

Query

10: 11: 12: 13: 14: 15: 16: 17:

sp_vertebrate:* sp_virus:*

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

89

15.2 15.2 15.1 14.9

68 67.5 67.5 67.5 67.5 67.5 67.5 67.5

491 491 491 1000 1018 1090 1214 296 307 478

Q9Y6M7

Q9NBK9

Q9nbk9

drosophila

Q9FT49

40444

14.8 14.8 14.8

Q9FGA8 O43651 Q96B56 Q9BQ31 Q9TT17 Q9TT19 Q9UIB9

۲.

Total number of hits satisfying chosen parameters:

671580 seqs, 206047115 residues

671580

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pecember 8, 2002, 18:34:08 ; Search time 57.2516 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAILTLSLQLILLLIPSISH......TSAGLTLQDLQLWCNLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (without alignments)
313.111 Million cell updates/sec
                                                                                                   Q9ddz5 brachydanio
Q88282 snakehead r
Q9fbj7 thermoplasm
Q9fda8 arabidopsis
Q43651 homo sapien
                                                                                                                                                                  Description
                                                                      Q9bq31
Q9tt17
                              Q9hc88
Q9y6m7
                                                                                           Q96b56
Q9x2g7 thermotoga
Q9ft49 arabidopsis
Q71146 human immun
                                                   1 homo sapien
7 oryctolagus
9 homo sapien
0 homo sapien
                                homo sapien
homo sapien
                                                                                           homo sapien
                                                                                            Q9DDZ5
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
                                                                                         The property of a TNF receptor and two TNF receptor and two TNF receptor and two TNF receptor and two TNF receptor in the fish ovary. ";

RT ligands in the fish ovary. ";

RT LComp. Blochem. physiol. B, Comp. Blochem. 129:475-481(2001).

DR HSSP, P50591; 1D0C.

R LFIN. 2DB-GENE-010801-1; tnfsf101.

DR HSSP, P50591; 1D0C.

R InterPro; IPR003658; TNF-abc: 1.

R InterPro; IPR000478; TNF-family.

R Ffam; PF00029; TNF; 1.

R PAST; SM00207; TNF; 1.

R SMART; SM00207; TNF; 1.

R SMART; SM00207; TNF; 1.

R SMART; P50039; TNF-2; 1.

R SMART; P50049; TNF-2; 1.

R SMORT; P550049; TNF-2; 1.

R SMORT; P550049; TNF-2; 1.
            g
                               δõ
                                                             Query Match
Best Local S
                                                     Matches
                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Cypriniformes;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TIEMBLIEL 16, 01-MAR-2001 (TIEMBLIEL 16, 01-MAR-2002 (TIEMBLIEL 20,
                                                                                                                                                                                                                                                                                                                                                                                 Q9DDZ5
                                                                                                                                                                                                                                                                                                                                                                      Q9DDZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5
63.5
63.5
63.5
63.5
                                                     Local Similarity
les 15; Conserv
            76 HOSCRHPVHTWANKSEGAHLYNWTLTNGRLRVPODGRYYLYSOVYFRY 123
                                20 HEAHKTSLSSWKHDODWANVSNMTFSNGKLRV--KGIVYRNADICSRH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.3
14.3
14.2
14.2
14.2
14.2
14.2
14.2
14.1
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14.0
13.8
13.8
13.7
13.7
13.7
13.7
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                       15.2%; Score 69; DB 13; Length 214; illarity 31.2%; Pred. No. 2.9; Conservative 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
427
1485
1562
262
297
561
813
813
287
345
156
246
2246
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212
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O46867
O O49734
6 Q8RFS0
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Q9X6N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VUN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VCJ9
Q8YPE8
Q913X9
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Q9FAC1
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Q972X5
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                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                             214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04974 arabidopsis
04974 arabidopsis
088750 fusobacteri
098750 fusobacteri
097861 streptomyce
097130 clostridium
097135 sulfolobus
09729 bacillus ha
09899 bacillus ha
099144 caenorhabdi
099144 saguinus oe
089907 saguinus oe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9g982 allomyces a
Q46867 ictalurus p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9vun0_drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8ype8 anabaena sp
Q9i3x9 pseudomonas
Q90wt9 gallus gall
Q8uia0 agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9c6r2 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9fac1 streptomyce
Q9vcj9 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8xtz4 ralstonia s
Q96z32 sulfolobus
Q96zt5 sulfolobus
Q9m393 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8sq08 saimiri sci
Q8w109 chlamydomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9hdg3 pneumocysti
Q9hex9 pneumocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9vj73 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q942b1 oryza sativ
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A KAWASHIMA T., AMANO N., KOIKE H., Makino S.-I., Higuchi S., A Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., A Kawashima T., Yamamoto K., Yamazaki M., Kanahori K., Kawamoto Y., Aramaki H., Makino K., Suzuki M.; Proc., Nathaeal adaptation to higher temperatures revealed by genomic Sequence of Thermoplasma volcanium."

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

PRIBL; APO00992: BAB59600, 1.

PROSITE: PS00572: GLYCOSYL. HYDROL_E1_1; UNKNOWN_1.

SQ SEQUENCE 1171 AA; 132418 MW; D347291D8573E6BE CRC64;
                         Matches
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            Q97BJ7
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
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Q88282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                    STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
                                                                                                                                                                                                                                                                   Thermoplasma volcanium.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
                                     Local
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Thermoplasmataceae; Thermoplasma
                                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein TV0458.
                                                                                                                                                                                                                                                              NCBI_TaxID=50339;
                                                                                                                                                                                                                                                                                                                                                                                               097вJ7
                                                                                                                                                                                                                                                                                                                                                                                                                                             532 TKTLKTGVTWTTAVVKIDLQQWVDI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hart D., Frerichs G.N., Rambaut A., Ronalds R.J., Onions D.E., Evidence for a new retrovirus genus of piscine origin.", Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U26458; AAC54858 J. E. EMBL/GenBank/DDBJ databases.
SEQUENCE 1130 AA, 128317 MW. B6A4F8095E4F0D3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476 SSGNSWKAEIDKIRKOKW----OKCYFSGKLRIKGTDYEBIDTCPKPLIGPLSGFIPTGV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96211493; PubMed-8648695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 TSLSSWKHD-----QDWANVSNWTFSNGKLRVKGIYYRNADICSRHRV-----TSA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hart D., Frerichs G.N., Rambaut A., Onions D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence and transcriptional analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=40270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Snakehead retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TremBirel
01-DEC-2001 (TremBirel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q88282;
Q88282;
            23: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol. 70:3606-3616(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retroid viruses; Retroviridae; Epsilonretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
       15.1%; Score 68.5;
27.1%; Pred. No. 2;
ative 17; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2%; Score 69; DB 15; Length 1130; 25.9%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                             PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1130 AA.
                      DB 17; Length 1171;
32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
13;
                                                                                                                                                              Kawamoto
Gaps
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043651
                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                                                                                                                                                                                             Db
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                                                                                                                                                                                                                                                                                                                                                                                                                           DЪ
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EMBL; AP043472; AAC13164.1;
InterPro; IPR000210; BTB POZ.
InterPro; IPR001522; K+channel_pore.
InterPro; IPR003971; Kv_channel.
InterPro; IPR003968; Kv_channel.
     InterPro; IPR003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                     "Electrically silent potassium channel subunits from human lens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                          MEDLINE=99413882; PubMed=10484328; Shepard A.R., Rae J.L.;
                                                                                                                                       TISSUE=LENS EPITHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ϋ́
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                   Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Shab-related delayed-rectifier K+ channel alpha subunit.
                                                                                                                                                                                                                                                                                                 043651;
                                                                                                                                                                                                                                                                                                                                                                 159 TLQMEQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

SEQUENCE 187 AA; 20056 MW; 305781D3A0738AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           102 HDAYVGILASLKSALLELKDSPDTANYDVMVSGDDTRRVKGLVEKNTDTASK---TLMEM 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Similarity to pollen-specific protein Bnml.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                         73 TLODLOL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                  20 HEAH-----KTSLSSWKHDQDWANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FGA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        942 YPKNLTSLVITINGLRLRCEADFIN 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       885 LWEPALGHYVLNFTYVTKTSNWINNTLYANLSNYAPAIYLKISNRDL--NGSYYLHI-LA 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 SRHRVTSAGLTLQDLQLWCNLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 LLIPSISHE----AHKTSLSSWKHDQDWANVSN-----MTFSNGKLRVKGIYYRNADIC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
K_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                             491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels
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DR SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96B56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.8%; Score 67.5; DB 4; Length 491; Best Local Similarity 22.0%; Pred. No. 12;
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                                                                                                         Q9BQ3
BEBBBBBB
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pram; Pr00520; ion_trans; 1.
Pram; Pr02214; K_tetra; 1.
PRINTS; PR01494; KV9CHANNEL.
PRINTS; PR01494; KV9CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003131; K_tetra.
InterPro; IPR000636; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ionic channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
potassium voltage-gated channel, delayed-rectifier, subfamily S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q96B56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISWTTVGYG------ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00520; Pfam; PF02214;
                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001622; K+channel_pore.
Interpro; IPR003131; K_tetra.
Interpro; IPR000636; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC015947; AAH15947.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
           Q9BQ31 PRELIMINARY; PRT; 491 AA.
Q9BQ31;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-3002 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGIY 55
                                                                                                                                                                                                                                     328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG------ 374
delayed-rectifier,
                                                                                                                                                                        375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                     56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                  1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGIY 55
                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                     491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                    K_tetra;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55970 MW; FFF12CA3CDA50185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       tra; 1.
56047 MW;
   subfamily S, member 3).
                                                                                                                                                                                                                                                                                                                     14.8%; Score 67.5;
22.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                       185D80646109C629 CRC64;
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA
                                                                                                                                                                                                                                                                                                                                          DB 4; Length 491;
                                                                                                                                                                                                                                                                                                           30; Indels
                                                                                                                                                                                                                                                                                                                25;
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DE GN OS OS OS OS RN RN RP RC RA RL DR RL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BBBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00520; ion_trans; 1.
Pfam; PF002214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01492; KV9CHANNEL.
PRINTS; PR01494; KV9CHANNEL.
PRINTS; PR01495; SHABCHANNEL.
PRINTS; PR01495; SHABCHANNEL.
PRINTS; PR01496; SHAWCHANNEL.
SMART; SM00225; BTB; 1.
SMART; SM00225; BTB; 1.
SEQUENCE 491 AA; 55984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC004987; AAH04987.1; -. EMBL; BC004148; AAH04148.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                           InterPro; IPR000210; BTB_POZ.
InterPro; IPR001672; K+channel_pore.
InterPro; IPR003971; Kv9_channel.
InterPro; IPR003978; Kv_channel.
InterPro; IPR003998; Kv_channel.
InterPro; IPR003991; K_channel.
InterPro; IPR003131; K_ctara.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_ctarnel_n1g.
InterPro; IPR00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003971;
InterPro; IPR003968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9TT17 PRELIMINARY; PKT; 431 AA.

O9TT17;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Voltage-gated delayed-rectifier potassium channel Kv9.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Ciditaca, Verconia, E
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                              Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                 STRAIN-NEW ZEALAND WHITE; TISSUE-CORNEA ENDOTHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCNS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG-----
                                                                                                                                                                                                                                                EMBL; AF209723; AAF22833.1;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
      Pfam; PF02214; K_tetra; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTFSNGKLRVKGIY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003974; Shaw_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K_channel.
K_tetra.
M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55984 MW; A5F12BF077A50DAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BTB_POZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K+channel_pore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 67.5;
22.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kv_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kv9_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 red. No. 12;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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                                                                                                                                                                                                                                                                                                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                   Sodium bicarbonate cotransporter2.
                                                                                                                                                                                                                                                     060350;
                                                                                                                                                                                                                                                                                 060350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02730; 1BNX.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001020; HCO3_cotransp.
Pfam; PF00955; HCO3_cotransp.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0834; ae; SEQUENCE 1000 AA; 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of a HCO3 transporter, NT2-NBC, from human brain, similar to both the Anion exchangers (AEs) and the Na/Bicarbonate Cotransporters
                                                                                                                                                                                                                                                                                                                                                                                                                      606 YIPDVLFWC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 PNPSNE----TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF053755; AAF21720.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 TLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bicarbonate transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Romero M.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UIB9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UIB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00169; KCHANNEL.
PRINTS; PR01494; KV9CHANNEL.
PRINTS; PR01491; KVCHANNEL.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 -----DTHPVTLAGKLIASTCIICGILVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWW-----WATISMTTVGYG----- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ionic channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 YRNADICSRHRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAILTLSLQLILLLIPSISHEAHKTSLSS-----WKHDQDWANVSNMTESNGKLRVKGTY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 AA; 55941 MW; 2EE396E0889D6F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 67.5; DE 31.9%; Pred. No. 27; ative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112501 MW; 93FAA40A3141F8F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 67.5; DB 6; Length 491; 22.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                  1018 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                         PRINTS; PRO1231; HCOSTRNSPORT.
TIGREAMS; TIGRO0834; ae; 1.
SEQUENCE 1090 AA; 123080 MW; 541839CC9B565896 CRC64;
                                                                                                                                                                                                            InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotransp.
Pfam; PF00955; HC03_cotransp; 1
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9HC88;
01-MAR-2001 (TIEMBLrel. 16, Created)
01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
Sodium bicarbonate cotransporter 2b.
696 YIPDVLFWC 704
                                             648 PNPSNE----TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 695
                                                                                                                                                                                                                                                                                 EMBL; AF089726; AAG
HSSP; P02730; 1BNX.
                                                                                                                                                                                                                                                                                                               Submitted (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                Pushkin A., Abuladze N., Newman D., Hwang J., Kurtz I.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              TISSUE-KIDNEY
                                                                             16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9нс88
                                                                                                                                                                                                                                                                                                                               Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete
                              73 TLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003920; HC03_cotransp.
Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
TIGREAMS; TIGR00834; ae; 1.
SEQUENCE 1018 AA; 114204 MW; A37799D93A1E30BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 0:0-0(1998). EMBL; AB012130; BAA25898.1; -. HSSP; P02730; 1BNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 YIPDVLFWC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558 PNPSNE----TLAQWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ishibashi K., Sasaki S., Marumo F.;
"Molecular cloning of a new sodium bicarbonate cotransporter cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-RETINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 TLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 67.5; DB 4; Length 1 ilarity 31.9%; Pred. No. 28; Conservative 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                              1998) to the EMBL/GenBank/DDBJ databases
                                                                                                            14.8%; Score 67.5; DB 4; Length 1090;
31.9%; Pred. No. 30;
tive 14; Mismatches 18; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1090 AA
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                                                                                                                15;
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RESULT 12 Q9Y6M7

Q9Y6M7

PRELIMINARY;

PRT;

1214 AA.

01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sodium bicarbonate cotransporter 3.

Homo sapiens (Human) Eukaryota; Metazoa;

; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

MEDLINE=99278433; PubMed=10347222;

TISSUE-SKELETAL MUSCLE; SEQUENCE FROM N.A.

"Cloning, tissue distribution, genomic organization, and function characterization of NBC3, a new member of the sodium bicarbonate

EMBL; AF047033; AAD38322.1; HSSP; P02730; 1BNX.

InterPro; IPR001717; Anion_exchange. InterPro; IPR003020; HCO3_cotransp.

cotransporter family."; J. Biol. Chem. 274:16569-16575(1999).

Pushkin A., Abuladze N., Lee I., Newman D., Hwang J.,

and functional

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OPT19
ACCOMENDED TO SEPT 19
ACCOMEND TO SEPT 19
AC
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FT49;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 34.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress). Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosid Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FT49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 BEDWEKFGGVPNVVFSDAMIBYNGYYYVYYGAADNC----IALATIPVEKVMKWC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL132972; CAC07924.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 DODW---ANVSNMTFSNGKLRVKG---TYYRNADICSRHRVTSAGLTLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     071146 PRELIMINARY:
071146; TrEMBLTel. 01,
01-NOV-1996 (TrEMBLTel. 01,
01-NOV-1996 (TrEMBLTel. 01,
01-DEC-2001 (TrEMBLTel. 01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 HDEYKVLSFIWRHNKEWKVRSEHHVLVLGARTSWKKTQCHIHHLPYSQG-ITINGVLYYG 207
                                                                                                                                                                                                                                                                                                                                                                                                    Envelope glycoprotein gp120 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                                                                                                                                                              Viruses; Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11676;
                                                                                                          Quinones-Mateu M.E., Dopazo J., Este J.A., Rota T.R., Domingo E., "Molecular characterization of human immunodeficiency virus type isolates from Venezuela.";
                                                                                                                                                                                         MEDLINE=96093896; PubMed=7576917;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 HEAHKTSLSSWKHDQDW---------ANVSNMTFSNGKLRVKGIYYRN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis sequencing project;
     STRAIN-VE2;
                             SEQUENCE FROM N.A.
                                                                               AIDS Res. Hum. Retroviruses 11:605-616(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWTDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADICSRHRVTSAGLTLQDLQLW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%; Score 67; DB
27.3%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34863 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%; Score 67; DB
18.3%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                            Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DC8746CB47D8F92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                Este J.A., Rota T.R., Domingo E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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RESULT 13
CO9X2G
ID O9X2G
AC O9X2G
DT 01-NC
CO Hact
CO Bactr
CO Ba

Hypothetical protein; Complete proteome. SEQUENCE 296 AA; 34197 MW; 11B3960CA5C3D2C6 CRC64;

밁 õ 뭥 Š

820 YIPDVLFWC 828

73 TLQDLQLWC 81

01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein TM1852,

Last annotation update) Last sequence update)

Created)

Thermotoga maritima

Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

NCBI_TaxID=2336;

Q9x2G7

PRELIMINARY;

296 AA.

Q9X2G7;

Matches Query Match

Local

Similarity

Conservative

772 PNPSNE----TLAOWKKDNITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 819

16 PSISHEAHKTSLSSWKHDQDWA-NVS--NMTFSNGKLRVKGIYYRNADICSRHRVTSAGL 72

14; Mismatches

18; Indels

Gaps

6,

14.8%; Score 67.5; DB 4; Length 1214; 31.9%; Pred. No. 34;

TIGREAMS; SEQUENCE

PION; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
PRINTS; PR01231; HCO3TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
SEQUENCE 1214 AA; 136042 MW; EF203500B5BF5267 CRC64;

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317
 21 AAY84417
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OM protein - protein search, using sw model Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Run on: December 8, 2002, 17:26:33; Search time 41.2387 Seconds Sequence: Searched: JOBATO Seqs, 133250620 residues JOBATO Total number of hits satisfying chosen parameters: JOBATO Total number of hits satisfying chosen parameters: JOBATO Search 1008 MAXImum bB seq length: JOBATO Sequence 4, 1008 MAXIMUM bB seq leng	
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score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

SUMMARIES

20 10 10 10 10 10 10 10 10 10 10 10 10 10	Result
358 178 178 178 178 178 178 178 178 178 17	Score
96.0 47.7 47.7 47.7 47.7 47.7 47.7 47.7	Query Match Length DB
95 152 160 244 244 246 246 317 317 317	ength [
23 22 21 23 23 19 19 19 19)B ID
AAU83632 AAB67248 AAB08273 AAU86148 AAU78286 AAW83020 AAW83195 AAW83018 AAW83018 AAW69957 AAW68293	Ð
Human RANKL. Homo Amino acid sequenc Amino acid sequenc Human pRO206 polyp Human TRANCE prote Osteoclastogenesis Human osteoprotege Osteoclastogenesis NF-KB receptor act	Description Human PRO protein,

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	AAY8	AAY8	AAB8	AAM4	AAOL	AAO /	MALO	27.6	AAY8	AAY91	AAY17	AAWS	AAWBS	AAWBS	ANE OF	1001	DAFO4	AAE08	AAW68	AAW69	AAWOS	TAL OF	1 1 1 1 1 1	AAY84	AAY844	AAY844	AAY844	AAB082	AAY910	AAY 1 / B	OZ SHA	10000	AU / 0 4	170	BB081	AAE01993	AE044	AE0873	WI O 4 4 7

Amino acid sequenc Human receptor act Human receptor act Human full-length Murine receptor ac Murine receptor ac Murine RANKL (rece Human osteoprotege Human RANKL polype Human TRANCE prote Mouse OBM protein Amino acid sequenc Amino acid sequenc Mouse FLAG-murine Rat osteoclast dif Amino acid sequenc An osteoprotegerin A murine OCIF-bind DNA encoding osteo An osteoprotegerin Human TRANCE. NF-kB receptor act Amino acid sequenc Amino acid sequenc Mouse TRANCE prote Amino acid sequenc Murine TRANCE. Mu Osteoclastogenesis Amino acid sequenc A murine osteoprot An osteoprotegerin GlutathioneStransf Murine GST-mODF fu Mouse OBM protein Hom

ALIGNMENTS

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ARBSULT 1
AAU636332
ID AAU64
AC AAU64
AC AAU64
AC AAU66
XX AAU66
XX Hume
AX Hume
KW bree
KW tum
XX Hum
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XX Hum
XX Hum
XX 29
PN WO2
PN W22
PN 25
PR 255
20-JUL-2000: 2000US-219556P.
25-JUL-2000: 2000US-220685P.
25-JUL-2000: 2000US-220607P.
25-JUL-2000: 2000US-220607P.
25-JUL-2000: 2000US-220624P.
25-JUL-2000: 2000US-220638P.
25-JUL-2000: 2000US-220664P.
25-JUL-2000: 2000US-220666P.
25-JUL-2000: 2000US-220893P.
26-JUL-2000: 2000US-220893P.
28-JUL-2000: 2000WO-US20710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; breast cancer; prostate tumour; chondrocyte cell proliferation; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU83632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO protein, Seq ID No 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208288-A2.
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                    CC encoding PRO polypeptides. The sequences of the 122 PRO polypuctions of the 220 proteins acids caponists and antagonists are useful for treating a PRO polypuctionists are useful for treating a PRO related disorder. CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or cc proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, cc stimulating or inhibiting the proliferation of continuous transported for stimulating or inhibiting the proliferation of normal human dermal cc weight markers and for tissue typing. The PRO nucleic as molecular cc and in chromosome and gene mapping. AAU83592-AAU83713 represent human procession for the sequences of the invention.
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Homo sapiens.
          Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
                                                           Human RANKL
                                                                                    18-APR-2001
                                                                                                                            AAB67248 standard; protein; 152 AA.
                                                                                                                  AAB67248;
                                                                                                                                                                                                        80 WCNLRSV 86
                                                                                                                                                                                                                                  61 WCNLRII 67
                                                                                                                                                                                                                                    20 HEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2000; 2000WO-US23522

24-AUG-2000; 2000WO-US23328

15-SEP-2000; 2000US-000000P

10-NOV-2000; 2000WO-US30873

28-NOV-2000; 2000WO-US30873

01-DEC-2000; 2000WO-US32678

20-DEC-2000; 2000WG-0747259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Figure 82; 359pp; English.
                                                                                                                                                                                                                                                  1 HEAHKTSLSSWKHDQDWANVSNMTESNGKLRVKGIYVRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-172001/22.
                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK33576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2000;
                                                                                                                                                                                                                                                                                                                  65;
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                             Conservative
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C, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US34956
2001WO-US06520
2001US-0854280
2001WO-US17092
                                                                                                                                                                                                                                                                                                                     96.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen ME, Goddard A, Godowski p
Smith V, Stephan JF, Watanabe CK,

    Mismatches

                                                                                                                                                                                                                                                                                             Score 358; DB 23; Length 95; pred. No. 2.3e-39; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood WI;
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AAB08273
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g.
                                                 WPI; 2000-558217/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                           Boyle WJ,
                                                                                                                     12-FEB-1999;
18-NOV-1999;
                                                                                                                                                11-FEB-2000; 2000WO-US03653.
                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                            17-AUG-2000.
                                                                                                                                                                                               WO200047740-A2.
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                               AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor;
                                                                                                                                                                                                                                 type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                    Amino acid sequence of a human TNF ligand QPGL.
                                                                                                                                                                                                                                                                                                                04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                              AAB08273;
                                                                                                                                                                                                                                                                                                                                                         AAB08273 standard; Protein; 160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation of the treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications -
                                                                                                                                                                                                                                                                                                                                                                                                 17 SHKYSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-123012/13.
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O'Connell M,
                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conserv
                                                                        Hsu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AA;
                                                                                                                  99US-0166271
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                            9908-0119906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hymowitz S, Kelley
Pai R, Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0141342
                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%; Score 178; DB-22; Length 152; 60.0%; Pred. No. 2.2e-15; tive 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kelley RF, Koumerokh Z, Simmons L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koumenis I,
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAHO8265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand specification describes an AGP-3 polypeptide, which is TNF ligand factor family member. AGP-3 is a type II transmembrane protein, and is a increase in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat AGP-3 proteins, antibodies, and nucleic acids may be used to replace, e.g. rheumatoid arthritis, inflammatory and immune disorders, e.g. rheumatoid arthritis, crohn's disease, lupus and graft versus host disease. The nucleic crohn's disease, lupus and graft versus host disease. The called acids may be used to replate the expression of a AGP-3 related acids may be used to replate the expression of an AGP-3 related useful for the detection of AGP-3 agonists, antagonists and useful for the detections with AGP-3 related proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU86148 standard; Protein; 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU86148;
                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disordaemia; neuronal disorder; immune disorder; angiogenic disorder; inflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO206 polypeptide:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                    WO200153486-A1.
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-2000;
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                                                                                                                                                                                                                                                           08-MAR-1999;
11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1999;
                                                                                                                                                                                                                                               11-MAY-1999;
                                                                                                                 01-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                              20-JUL-1999;
                                                                                                                                                                                                         22-JUN-1999;
                                                                                                                                                                                                                      22-JUN-1999
                                                                                                                                            31-AUG-1999;
                                                                                                                                                                                 26-JUL-1999;
                                                                                                    30-NOV-1999
 Marsters SA,
                                      (GETH ) GENENTECH INC.
              Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                     2000WO-US03565.
                                                                    2000WO-US00219
       Pan J,
                                                                                                                                                                                                                                                    99US-133459P
                                                                                                                                                                                                                                                               99US-123972P.
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                                                                                                                                                                                                               99US-140653P.
                                                                                                                                                                                                                                          99WO-US1
                                                                                                                        99WO-US21090
                                                                                                                                     99WO-US20111
                                                                                                                                                99US-
                                                                                               99WO-US28301.
                                                                                                          99WO-US28313.
                     Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.78;
                                                                                                                                                     151689P.
         Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DB 21;
pred. No. 2.4e-15;
5; Mismatches 17;
            Godowski PJ, Gurney AL,
i RM, Roy MA, Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                            blastocoelic disorder;
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                  Stone DM;
                                  Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides and the polynucleotide sequences encoding them. The propertides, agonists, antagonists or anti-pRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABK40274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 61; Fig 42; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU78286 standard; Protein; 244 AA
                                                                                                                                                                                                                                                                                                                                                                                       TRANCE, dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; heumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; rheumatoid arthritis; acromegaly; gigantism; exostosis; chondrocyte; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU78286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 SHKVSLSSWYHDRGWAKISNWTFSNGKLIVNODGFYYLYANICFRHHETSGDLATEYLQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour necrosis factor-related activation induced cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TRANCE protein splice variant 2.
                                                                                                                                                                                                                                                                                                                WO200216551-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           cartilage growth; skeletal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                      (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                                                                                                                   18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                  20-AUG-2001; 2001WO-US26101.
                                                                                                                                                                                                                                                                                   28-FEB-2002
                                            Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-205567/26.
                                                                                                            N-PSDB; ABK12877
Disclosure; Fig 4; 55pp; English.
                              cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                               2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 AA;
                                                                                                                                                          Odgren PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%;
                                                                                                                                                                Marks SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 178; DB 23;
Pred. No. 4.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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RESULT 6
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Example 28; Pages 119-120; 151pp; Japanese.
                                              Protein binding to osteoclastogenesis inhibitory factor - useful
                                          calcium metabolism
                                                                                                             WPI; 1998-594563/50.
                                                                                                                                    Nakagawa N, Shima N, Tai
Washida N, Yamaguchi K,
                                                                                                                                                                                                                                              02-DEC-1997;
15-APR-1997;
09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 36;
                                                                                                                                                                                       (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                 15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                        W09846644-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW83020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW83020 standard; Protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 SHKVSLSSWYHDRGWAKISNMTESNGKLIVNQDGFYYLYANICERHHETSGDLATBYLQL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and acts directly on cartilage-producing cells (chondrocytes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADIGSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                   AAV69899
                                                                                                                                                     Higashio K,
1 N, Shima N,
                                      treatment and investigation of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 AA;
                                                                                                                                                                                                                                     97JP-0097808.
97JP-0151434.
97JP-0217897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                       97JP-0224803
                                                                                                                                                                                                                                                                               97JP-0332241.
                                                                                                                                                                                                                                                                                                           98WO-JP01728.
                                                                                                                         Kinosaki M, Kobayashi F,
Takahashi K, Tomoyasu A,
i K, Yano K, Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178; DB 23;
Pred. No. 4.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                   of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intermediate of the protein in the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an osteoclastogenesis inhibitory factor (CCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone. CC absorption factors such as calcitriol or parathyroid hormone (PTH). CC absorption factor by separation and solubilisation of membrane proteins cC then affinity chromatography using OCIF. It exists in a full-sequence cC used for screening potential inhibitors and modifiers of its biological cC activity, and screening for receptors to OBM which mediate its function. CC of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                             Claim 19; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                         Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV70285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1998;
16-APR-1997;
23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-594578/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09846751-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoprosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human osteoprotegerin binding protein from the pcDNA/huOPGbpl.linsert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW83195 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW83195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 SHKVSLSSWYHDRGWAKISNWTESNGKLIVNQDGEYYLYANICERHHETSGDLATEYLQL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0052521.
97US-0842842.
97US-0880855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US07584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DB 19;
Pred. No. 4.2e-15;
5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 246;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation modulate binding of OPG binding protein con sociocast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding binding protein can be used to detect OPG binding protein encoding transgenic animal models, while complementary sequences are used for transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or activation of OPG binding protein. Soluble forms of OPG binding protein particularly soluble forms of OPG binding protein or b, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW83018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW83018 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1997;
15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1998;
           The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone OBM is isolated from stroma cells cultured in the presence of
                                                                                                                                                                                                                                                                                   Goto M, Higashio K, Kin
Nakagawa N, Shima N, Tak
Washida N, Yamaguchi K,
                                                                                                                                                                                                                                                                                                                                                          (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-1997;
                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                            protein binding to osteoclastogenesis inhibitory factor - useful
for, e.g. treatment and investigation of disorders of bone and
absorption factor by separation and solubilisation of membrane proteins
                                                                                                                            Claim 36; Pages 113-114; 151pp; Japanese.
                                                                                                                                                              calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POCET
                                                                                                                                                                                                                                                        1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
36; Conserv
                                                                                                                                                                                                                                        AAV69887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0151434.
97JP-0217897.
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                                                                                                                                                                                                                                                                                                                                 Kinosaki M,
                                                                                                                                                                                                                                                                                                              Takahashi K,
                                                                                                                                                                                                                                                                                           Yano K,
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Pred. No. 5.8e-15;
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                                                                                                                                                                                                                                                                                                                Kobayashi F,
, Tomoyasu A,
                                                                                                                                                                                                                                                                                                  Yasuda H;
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Tsuda E;
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        Query Match
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This represents a human RANKL, a ligand for the RANK (receptor CC activator of necrosis factor (RappaB (NF-kB)) polypeptide. RANK is a CC activator of necrosis factor (RMP) family. A soluble RANK CC member of the tumour necrosis factor (RMP) family. A soluble RANK CC member of the fumour necrosis factor (RMP) family. A soluble RANK CC may be used for inhibiting activated not of NF-kB, by contacting a cell cc expressing membrane-associated RANK with a soluble RANK and can be CC used to induce maturation of dendritic cells and enhance their CC used to induce maturation of dendritic cells and enhance their CC used to induce maturation of the cells and enhance their CC composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists immune or inflammatory response. Inhibition of NF-kB by RANK antagonists immune or inflammatory response. Inhibition of NF-kB by RANK antagonists immune or sepsis, graft-versus-host reactions, or acute inflammatory cc reactions. They can also be used in adjunct therapy for disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be form screening potential inhibitors and modifiers of its biological used for screening for receptors to OBM which mediate its function. activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay function and calcium metabolism. The antibodies can be used for assay function and calcium metabolism. The antibodies can be used for assay function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                components of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW69957 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 SHKYSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANKL; RANK ligand; tumour necrosis factor; TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1997;
                                                                                                                                                                                                                                                                                                                             New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                            Claim 27; pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-377657/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ა
6;
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                                                                                                                                                                                                                                                                                                                                                                                                               AAV41378.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galibert LJ, Maraskovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0059978.
97US-0813509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0064671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US23775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 178; DB 19;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor kappaB (NF-kB)) polypeptide. RANK is a CC member of the tumour necrosis factor (TNF) family. Host cells transformed to runsfected with an expression vector comprising the RANK encoding CC nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CC used for regulating an immune or inflammatory response. Inhibition of CC NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in inflammatory reactions. They can also be used in adjunct therapy for consists can also be used in adjunct therapy for can also be used for detection and drum account.
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can also be used for detection and drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                      Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                            New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or
                                                                                                                                                                                                                                                                                 inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV41372
                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; infiammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09828424-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW68293 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 SHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Galibert LJ, Maraskovsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.78;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                               useful
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                The present sequence represents a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoplastogenesis in a dose dependent protein. The OPGL protein is synthesised as a type II transmembrane is a potent osteoplast differentiation factor when combined with CSF-1. Of CSF-1. OPGL is also an activator of mature osteoplast differentiation factor when combined with CSF-1. of CSF-1. OPGL is also an activator of mature osteoplasts. The opgl activaty in an animal. The method comprises using at least one OPGL activaty in an animal. The method comprises using at least one OPGL an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other alicenses.
         diseases or conditions characterised by excessive bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                           Claim 19; Page 78-79; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                      to treat, prevent and ameliorate osteoporosis
                                                                                                                                                                                                                                                                        In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ99964
                                                                                                                                                                                                                                                                                                                                                                          Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W0200015807-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response; osteoporosis; bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY84417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                        2000-271444/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0102896
                                                                                                                                                                                                                                                                                                                                                                                                                                                 98DK-0001164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "extracellular stalk domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.78;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "active ligand moiety"
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Pred. No. 5.8e-15;
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Sequence

317 AA;

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Ax The patent discloses novel receptor activator of nuclear factor (NF)-
CC kappaB (RANK) proteins and their corresponding DNAS. RANK is a member
CC with TNF receptor associated factor (TNF) receptor superfamily and associates
CC with TNF receptor associated factor (TNF) and 3 which are important
CC in the regulation of immune and inflammatory response. The receptors
CC are useful for regulating immune response and in screening for inhibitors
CC of these receptors. The cytoplasmic domain of RANK is used in developing
CC of these receptors of signal transduction, e.g. for screening the
CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
CC response that result from triggering of RANK, e.g. in treating toxic
CC are useful in ameliorating the negative effects of an inflammatory
CC shock or sepsis, graft-versus-host reactions, acute inflammatory
CC shock or sepsis, graft-versus-host reactions, acute inflammatory
CC apoptotic signal and rescue the cells that express RANK from apoptosis.
CC soluble forms of the receptor are used in vivo or in vitro based
CC soluble forms of the receptor are used in vivo or to inhibit
CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAP; tumour necrosis finflammatory response; graft-versus-host reaction; immune response; inflammatory response; profit bone resorption; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE08738 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human receptor activator of NF kappaB ligand (RANKL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE08738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 SHKVSLSSWYHDRGWAKISNWIFFSNGKLIVNODGEYYLYANICFRHHETSGDLATEYLOL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1997;
23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dougall WC,
                                                                                                                                                                                                                                                                                                                                                                                   New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                     Example 15; Column 71-72; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                       express RANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 47.7%;
Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-520313/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD15311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galibert L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0813509.
97US-0996139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0077181.
97US-0064671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0215649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0772330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0059978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178; DB 21; Length 317; pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast express and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are used as inhibitors of anti-inflammatory agents. The ranalysis useful for the expression of recombinant proteins, as probes for analysis useful in preparing kits for the detection of soluble RANK, or are useful in preparing kits for the detection of soluble RANK, or are useful in preparing kits for the detection of soluble RANK ligand monitor RANK related activity. The present sequence is RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RANKL) protein from human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE04426 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human receptor activator of NF-chi B ligand (huRANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6242213-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                    14-OCT-1997;
                                                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP.
                                                                                                                                       New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK)
The present invention relates to receptor activator of NF-chi B (RANK) to DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to Chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular
                                                                                                                                                                                                           N-PSDB; AAD08715
                                                                                                                                                                                                                                                                 Anderson DM
                                                                                                      Claim 1; Column 65-66; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                    2001-407216/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              97US-0995659
                                                                                                                                                                                                                                                                                                                                           97US-0064671
                                                                                                                                                                                                                                                                                                                                                                             96US-0059978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Receptor binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
162..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 22;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor). KappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I factors (TRAFS). Triggering of RANK by overexpression or co-expression of factors (TRAFS). Triggering of RANK by overexpression or co-expression or co-expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE01993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSSSXX
SSSSSXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 76-77; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD05904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson DM, Hughes AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2000; 2000WO-US31459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200136637-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human full-length RANKL (receptor activator of NF-kappaB ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE01993 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 SHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region, RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-329222/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9908-0442029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 22;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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CC from infection with a pathogenic or opportunistic organism. The method convolves administering a combination of two to five agents comprising:

CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation of two to five agents comprising:

CC agent; (c) dendritic cell activation agent; (d) Tocal antauration:

CC or (e) activated, antigen-specific Tocals. The methods are useful for treating an individual at risk for or suffering from infection with a composition or opportunistic organism, e.g. vituses (e.g. HIV), bacteria cruzi, which causes Chaga's disease). The methods are especially companied a lymphocyte-mediated immune response. In particular, the harpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, cepresents a human RANKL polypeptide fragment. The present sequence xx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB08134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                         The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism. The method
                                                                                                                                                                                                                                                                                                                                            Treating an individual suffering from infection, e.g. inflammation, chickenpox or AIDS, by administering a combination of dendritic cell antigen-specific T cells - reaturation agent, T cell enhancing factor and
                                                                                                                                                                                                                                                                                                                       Disclosure; Page 42-43; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-500114/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-2000; 2000US-245721P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lynch DH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-2001; 2001WO-US44834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W0200236141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial; fungicide; protozoacide; virucide; anti_inflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human RANKL polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB08134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB08134 standard; protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteolysis (FEO) and early onset Paget's disease of bone (EP). The Present amino acid sequence is full-length human RANKL (huRANKL) protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 SHKYSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTLQDLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Smedt TN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.78;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maliszewski CR, Butz EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 178; DB 22;
Pred. No. 5.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 317;
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Tue Dec 10 10:51:44 2002

Query Match

Query Match

Best Local Similarity 60.0%; Pred. No. 5.8e-15; Indels 2; Gaps 1;

Best Local Similarity 60.0%; Pred. No. 5.8e-15; Indels 2; Gaps 1, Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1, Mismatches 17; Indels 2; Gaps 1, Mismatches 17; Indels 2; Gaps 1, Indels 2; Gaps

saccharomyc

OM protein - protein search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

pecember 8, 2002, 17:28:38; Search time 16.2774 Seconds

(without alignments)
221.684 Million cell updates/sec

Run on:

Title:

Scoring table: Sequence: Perfect score:

BLOSUM62

1 MAILTLSLQLILLLIPSISH.....

TSAGLTLQDLQLWCNLRIIH 87

US-09-880-457-4

Post-processing: Minimum Match 0% Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Maximum Match 100% Listing first 45 summaries

Database

SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ŏ.

Score

Match Length DB

39.7

TN11_HUMAN

014788 h tumor Description

CSD2_DROME

p41922 yarrowia li p50365 allomyces m 084110 chlamydia t p29716 clostridium

Q9vmt6 drosophila

m tumor nec

Query

65

64

14.1 14.0 13.8

GUB_CLOTM PYRF_PICAN

Q06375 P45300

pichia angu haemophilus

sod

taurus

streptomyce

saccharomyc trichosurus

mycoplasma sulfolobus

escherichia anabaena sp streptomyce

escherichia saccharomyc saccharomyc YRAN_HAEIN Y108_CHLTR NU5M_ALLMA

61.5 61.5 63

60

329 1078 851 2144 1451 196 301 785

Y186_MYCPN APE2_SULSO

IPNS_STRCL CYA7_BOVIN NUD1_YEAST GLT1_YEAST SPT6_YEAST

58

216 329 561 220 958 1859 551 478 525 572 677 1856

PIS_YEAST AMYG_DEBOC GBF1_HUMAN

FIXN_AZOCA

agkistrodon azorhizobiu debaryomyce saccharomyc homo sapien

saccharomyc pisum sativ saccharomyc cricetulus

drosophila

ATKA_ANASL SGAH_ECOL1

IPNS_STRJU

Q9r6x2

58 57.5 57.5 57.5 57.5 57.5 57.5

DISR_AGKRH
ATF1_YEAST
GSHC_PEA
RN14_YEAST
GBBF1_CRIGR
RP1_HUMAN
CORZ_DROME

59.5 59.5 59.5

Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues Gapop 10.0 , Gapext 0.5

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RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
35
37
38
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41
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43
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CO14788; O14723; O9P2Q3; O96Q17;
CO14788; O14723; O9P2Q3; O96Q17;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Bone marrow, and peripheral blood; MEDLINE=98032977; PubMed=9367155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Lymph node;

MEDLINE=98227661; PubMed=9568710;

MEDLINE=98227661; PubMed=9568710;

Lacey D.T. Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,

Burgess T., Elliott R., Colombero A., Elliott G., Eli A., Qian Y.-X.,

Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,

Sullivan J., Hawkins N., Davy E., Capparelli G., Guo J., Delaney J.,

Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). Ikeda T., Kuroyama H., Hirokawa K.; "Determination of human RANKL isoforms.";
                                                                                                                                                                                                                                                                                                                                                                         differentiation and activation. Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                              "Osteoprotegerin ligand is a cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                 Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               SEQUENCE OF 73-317 FROM N.A.
                                                             Choi Y.; "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."; J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                            Wong B.R., Rho J., Arron J., Robinson E.
Kalachikov S., Cayani E., Bartlett F.S.
                                                                                                                                                                              MEDLINE=97460112; PubMed=9312132;
MEDLINE=97460112; PubMed=9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
    TISSUE=Tongue;
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1444
1585
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VP7_BPPH6
TEHB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRE6_YEAST
RRPL_RDVF
P3K3_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPNS_STRLP
FCG1_MOUSE
ISCS_METTE
GSHC_SOYBN
YSW1_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UL84_HCMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p32486 saccharomyc
Q98631 rice dwarf
p54675 dictyosteli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P19594
P11123
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P57795
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Q10017
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bacteriopha
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MEDLINE-20175237; PubMed=10708588;
Magai M., Kyakumoto S., Sato N.;
"Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF019047; AAB86811.1; --
EMBL; AF053712; AAC39731.1; --
EMBL; AB064269; BAB79694.1; --
EMBL; AB064277; BAB79695.1; --
EMBL; AB064270; BAB79695.1; --
EMBL; AF013171; AAC51762.1; --
EMBL; AB037599; BAA90488.1; --
                                                    SEQUENCE
                                                                CONFLICT
                                                                               VARSPLIC
                                                                                             VARSPLIC
                                                                                                           CARBOHYD
                                                                                                                         CARBOHYD
                                                                                                                                                      DOMAIN
                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                 Signal-anchor;
                                                                                                                                                                                                                                                                                    Cytokine;
                                                                                                                                                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                         PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                    ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its early non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00229;
                                                                                                                                                                                                                                                                                                                                                                                                MIM; 602642;
                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P50591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catalyzed by ADAM17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are produced by alternative splicing.

TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKCCYTES, BONE MARROW, HEART,
PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.

INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.

PTM: The soluble form of isoform 1 derives from the membrane for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypercalcenia of malignancy.
SUBUNT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
Secreted (isoform 2). A soluble form of isoform 1 arises by
Proteolytic processing (By similarity).
ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by proteolytic processing (By similarity). The cleavage may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Cytokine that binds to TNFRSFILB/OPG and to TNFRSFILA/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:11926; TNFSF11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     them. Biophys. Res. Commun. 269
FUNCTION: Cytokine that binds
                                                                                                                                                                                                                                                                                                            PS00251;
                                                                                                                                                                                                                                                        Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                IPR003636; TNF_abc
IPR000478; TNF_fam:
                                                                                                                                                                                                                        140
                                                                                                                                                 69
                                                                                                                                                                                                             Alternative splicing.

1 317 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
1 STREET TOWNS NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                       TNF;
                                                                                                                                                                                                                                                                                                 TNF_1; FALSE_NEG.
    39.7%; Score 180.5;
                                          35478 MW;
                                                                                                                                                                                                                                                                                                                                                               "NF_family.
                                            MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 2).
A -> G (IN REF. 4).
                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                    MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                           CLEAVAGE
                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                 MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                              766176446348097£ CRC64;
                                                                                                                     (BY SIMILARITY)
    DB 1;
Length 317;
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TN1
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EMBL; AF425669; AAL23963.1;
                           use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                         Marks S.C. Jr.,

"Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.",

Int. J. Dev. Bol. 45:853-859(2001).

-!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions regulation of the T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play
                                                                                                                              PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                           -!- SUBUNIT: Homotrimer (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                   Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-S
Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 59.7 Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11804028;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Fischer
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 266-318 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, sequence and functional characterization of the rathomologue of receptor activator of NF-kB ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zheng M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20540945; PubMed=11092398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Tibial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                  Similarity).
TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TN11_RAT
                                                                                                                                                                                                            an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone Miner. Res. 15:2178-2186(2000).
                 AF187319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 ATEYLOL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 IPSISHEAHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
       AAG17031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                             344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,
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                                                                                                                                                                                                                                                                                                                                                                                             MacKay C., Mason-Savas A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00251; TNF_1; FALSE_NEG. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWII_MOUSE STANDARD;

PRIY: 310 AA.

TWII_MOUSE STANDARD;

035235; 035306; 09R1V0; 09JJK8; 09JJK9;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 40, Casterian update)

15-JUN-2002 (Rel. 40, Casterian update)

15-JUN-2002 (Rel. 40, Last sequence update)

16-OCT-2001 (R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 IPSISHEAHKTSLSSWKHDODWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 PADYLQL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFSF11 OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 TLODIOL 79
                                                                                                                                                                                                                                                                                                    TISSUE-Hybridoma;
MEDLINE-97460112; PubMed-9312132;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                                                                                                                                                                                                                                                          Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                  "TRANCE is a novel ligand of the tumor necrosis factor receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00207;
                                                         Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tomotsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
                                                                                                  rissue-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
                                                                                                                                                                                 Biol. Chem. 272:25190-25194(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JSE STANDARD; PRT; 31
035306; Q9R1Y0; Q9JJK8; Q9JJK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
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140
199
264
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF_abc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
                                                                                                                                                                                                          c-Jun N-terminal kinase in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 11, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> M (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 177.5; DB pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4B87AAD706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
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TISSUE=Bone marrow;

MEDLINE=98227661; PubMed=9568710;

MEDLINE=98227661; PubMed=9568710;

Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,

Burgess T., Elliott R., Colombero A., Elliott G., Eli A., Qian Y.-X.,

Burgess T., Elliott R., Colombero A., Capparelli C., Eli A., Qian Y.-X.,

Sullivan J., Hawkins N., Davy E., Capparelli C., Guo J., Delaney J.,

Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation and activation.
Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M., Yasuda H., Shima N., Nakagawa N., Yano K., Goto M., Murakami A., Tsuda E., Wochizuki S. I. Tomoyasu A., Yano K., Goto M., Suda T., Wochizuki S. I., Higashio K., Udagawa N., Takahashi N., Suda T., Worinaga T., Higashio K., Udagawa N., Takahashi N., Suda T., "Osteoprotegerin/osteoclastof factor is a ligand for steeprotegerin/osteoclastogenesis-inhibitory factor and is identical osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Bone marrow stroma;
MEDLINE-98188248; PubMed-9520411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Osteoprotegerin ligand is a cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99214075; PubMed=10196481; Kodaira K., Kodaira K., Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ueda M., Higashio K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1; 2
MEDLINE=21150053; PubMed=11250921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ikeda I., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of nuclear
factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 230:121-127(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., schloendorff J., Tempst P., Choi Y., Blobel C.P., and schloendorff J., Tempst P., Choi Y., Blobel C.P., and schloendorff J., Tempst P., Choi Y., Blobel C.P., and schloender for a role of a tumor necrosis factor-alpha "Evidence for a role of a tumor necrosis factor-alpha of TRANCE, and the schloender of the schloender in the schloender of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         survival."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; Cam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; Cram J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; Cram J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; Control of the Transfer Terminants of the Teitelbaum S.L., Fremont D.H.; Cram T., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; Control of the Transfer Teitelbaum S.L., Fremont D.H.; Contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
                                                                                                                                                                                                                                                                                     J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
                                                                                                                                                                                                                                                                                                                                                                                   Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.; "Crystal structure of the extracellular domain of mouse RANK ligand
                                                                                                                                                                                                                                                                                                                                                         2.2-A resolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 274:13613-13618(1999).
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    proliferation. May be an important regulator of interactions proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play a important role in enhanced bone-resorption in humoral an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
                                                                                                                                                                                                    aiol. Chem. 277:6631-6636(2002).
FUNCTION: Cytokine that binds to INFRSF11B/OPG and to FUNCTION: Cytokine that binds to INFRSF11A/RANK. Osteoclast differentiation and activation factor. Therefila/RANK. Osteoclast differentiation stimulate naive T-cell augments the ability of immortant regulator of interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AND 3).
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Best Local fimilarity
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                           CONFLICT
                                                                                                                                                                                    SMART; SMUJZU, INC. 1.

PROSITE: PSO0251; TNF_1; FALSE_NEG.

CYTOKINE; PS50049; TNF_2; 1.

CYTOKINE; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor; 3D-structure; Alternative spilocing.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY CHAIN

CHAIN

139

316

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY COTTIBLE FORM.
                                                                                                    VARSPLIC
                                                                                                                                         CARBOHYD
                                                                                                                                                                  NIAMOG
                                                                                                                                                                                                                                                                                                         PDB; IIQA; 13-MAR-02

MGD; MGI:1100089; Tnfsf11.

InterPro; IPR003636; TNF-abc.

InterPro; IPR000478; TNF-family.

Pfam; PF00229; TNF; 1

SMART; SM00207; TNF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no many entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (180forms 1 and 2); Cytoplasmic (180form 3).
-!- ALTERNATIVE PRODUCTS: 3 150forms; 1 (shown here), 2 and 3; are produced by alternative splicing.
-!- FISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by proteolytic processing. The cleavage may be catalyzed by ADAMI?. A further shorter soluble form was observed.
DISEASE: DEFICIENCY IN THESTII RESULTS IN FAILURE TO FORM LOBULO-
ALVEOLAR MAMMARY STRUCTURES DURING PRECNANCY RESULTING IN DEATH
OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH NO OSTEOCLASTS, MARROW SPACES, OR TOOTH EROPTION, AND EXHIBIT THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MELETAL SITES, INCLUDING HYPERTROPHIC CHONDROCYTES.

WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRABECULAR BONE AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homotrimer
                                                316 AA;
                                                                           99
                                         34944 MW;
Pred. No. 4.4e-13;
             Score 176;
                                                MISSING (IN REF. 2)
                                                                      SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (IN
                                                                                                                                                           MEMBER 11 SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                             MISSING (IN ISOFORM 3)
                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                             08DF63A2BE00967A CRC64;
     Length 316;
                                                                                                    (POTENTIAL).
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RA Address M.D. Celniker S.E. Holt R.A. Evans C.A. Gocayne J.D. RA Admans M.D. Celniker S.E. Li P.W. Hoskins R.A. Golayne J.D. RA Admanstides P.G. Scherer S.E. Li P.W. Hoskins R.A. Galle R.F. RA Admanstides P.G. Scherer S.E. Li P.W. Hoskins R.A. Galle R.F. RA Gorge R.A. Lewis S.E. Richards S. Ashburner M. Henderson S.N. RA Sutton G.G. Wortman J.R. vandell M.D. Zhang Q. Chen L.X. RA Sutton G.G. Wortman J.R. vandell M.D. Zhang Q. Chen L.X. RA Ballew R.M. Basu A. An H.J. And H.G. Charpe M. Periffer B.D. RA Mark I.J. Doyle C. Baxter E.G. Richards Q. Chen L.X. RA Ballew R.M. Basu A. An H.J. And H.J. Andrews-Pfannkoch C. Bladwin D. Bayta N. Basu A. An H.J. Bandari D. Bolshakov S. R. Berman B.P. Bhandari D. Bolshakov S. R. Burtis K.C. Busam D.A. Butler H. Cadieu E. Dew I. Bolshakov S. R. Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P. Barder R. Davenport C. Center A. Chandra I. Davies P. Cawley S. Dahlke C. Davenport D. Bolshakov S. R. Burtis K.C. Busam D.A. Butler H. Cadieu E. Center A. Chandra I. Davies P. Cawley S. Dahlke C. Davenport L.B. Davies C. Barder R. Davis R. Cawley S. Dahlke C. Davenport L.B. Davies C. R. RA Glodek M. Gong F. Gorrell J.H. Cadieu E. Center A. Chandra I. Davies C. Burtis R. C. Gabriellan A.B. Garg N.S. Gelbart W. J. Dietz S.M. RA Harris N. L. Harvey D. Heiman T.J. Hernandez J.R. Harris M. Jalai M. Kalush F. Karpen G.H. Ke Z. Kennison J.A. Ketchum K.A. Howland T.J. Wei M. H. Diegwam C. R. A Lasko P. Lei Y. Levitsky A.A. Li J. Li Liang Y. Lin X. RA Lasko P. Lei Y. Levitsky A.A. Li J. L. Liang Y. Lin X. RA RA Malle B.E. McIntosh T.C. McLodd M.P. McPherson D.L. RA RA Malle B.C. Siden Kamos J. Singson M. Supsyski M.P. Welson K.D. Murphy B. Murphy L. Muzny D.M. Nelson M. R. RA RA Malle B.C. Siden R. N. Saunders R.D. C. Scheeler F. Shen H. RA Ra Mouth S. M. Wolsen K.S. Pan S. Pollard J. Puri V. Reese M.G. Shen B.C. Stapleton M. Stong K. Welssenbach J. Wang X. Ra Ra Mouth S. M. Wolsen R. D. C. Scheeler F. Shen H. Ra Ra Golden R. Wolle R. Wolsen R. Welssenbach J. Wang X. Ra Ra Ra Ra Ra Ra R
Nelson B.;
Unpublished observations (SEP-2000).
-!- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND
IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).
                                                                                                                                         CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSD2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Hexapoda;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable cytochrome P450 28d2 (EC 1.14. ---) (CYPXXVIIID2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSD2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 DYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 ŚIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNODGFYYLYANICFRHHETSGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 SISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC65_YARLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.
-i- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute as long as its content is in no way use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PlyBase; FBgn0031688; Cyp28d2.
InterPro: IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003609; AAF52225.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                privis; PRO0385; P450.

privis; PRO0385; CYTOCHROME P450; 1.

prosite; PS00086; CYTOCHROME P450; 1.

oxidoreductase; Monocytenase; Membrane; Heme; Microsome; Oxidoreductase; Monocytenase; Membrane; Horotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoplasmic reticulum; Hypothetical protein
BINDING 446 446 HEME (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               SEC65 OR SRP19.
Yarrowia lipolytica (Candida lipolytica)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC65_YARLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 KERRSEIMPALSPNRVKAVYPVSQSVCKKFVEYIRRQQQMATSEGLDAMDLSLCYTTEVV 192
                                                                                                                                                                                                                  Sanchez M., Beckerich J.M., Gaillardin C., Dominguez A., "Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a component of the yeast signal recognition particle displaying homology with the human SRP19 gene.";
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 20460 / W29;
MEDLINE-98085978; PubMed-9426009;
                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ------RVKGIYYRNADICSR------HRVTSAGLTLQDLQLWCNLRII 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 VGVFTTRVPQLLVMCPEYIHKIYATDFRSF-HNNEWRNFVNKKTDMILGNNPFVLTGDEW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene model prediction.
                                                      SRP54, SEC65, SRP21, SPR14 AND SRP7 (BY SIMILARITY).
                                                                                                                                                                                                        Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pocar
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                          e 203:75-84(199/).

EVINCTION: SIGNAL RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE FUNCTION: SIGNAL RECOGNITION THE ROUGH ENDOLASMIC REFICULUV IN TARGETING SECRETORY PROTEINS TO THE ROUGH ENDOLASMIC REFICULUP MEMBRANE. IT MUST BE INVOLVED INTIMATELY IN THE TRANSLOCATION OF A MIDE VARIETY OF PROTEIN SUBSTRATES (BY SIMILARITY). OF A 75 RNA SUBBUNIT: FUNGAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 75 RNA SUBBUNIT: FUNGAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 75 RNA SUBBUNITS: SRP72, SRP68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recognition particle SEC65 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ref.1
                                                                                                                                                                                                                                                                                                                                                                                                             Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%; Score 78.5; DB 1; Length 501; 20.0%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEME (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9AD85F249390A655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
'
                                                                                                                                                                                          RETICULUM
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NU5M_ALLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z22570; CAA80293.1; InterPro; IPR002778; SRP19. pfam; PF01922; SRP19; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal recognition particle; RNA-binding; Ribonucleoprotein. SEQUENCE 310 AA; 35487 MW; D65EC9F0C80114C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01922; SRP19; 1.
ProDom; PD006609; SRP19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50365;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NU5M_ALLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 MLTLPSI-YEAHKT-----HPKDWAN-----PGRVRVQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC 46923 / BURMA 3-35 (350C);
Paquin B., Roewer I., Wang Z., Lang B.E.;
"A robust fungal phylogeny using the mitochondrially encoded nad5 protein sequence.";
Can. J. Bot. 73:S180-S185(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Chytridiomycota; Blastocladiales; Blastocladiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ND5 OR NAD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allomyces macrogynus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=28583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                sequence from an ancestral fungus.";
J. Mol. Biol. 255:688-701(1996).
-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 46923 / BURMA 3-35 (350C);
MEDLINE-96226032; PubMed-8636971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                "The mitochondrial DNA of Allomyces macrogynus: the complete genomic
                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                           Interpro; ipR003916; NADHub_oxred5.
Interpro; ipR001750; Oxidored_q1.
Interpro; ipR001516; Oxidored_q1_N.
                                                                                                                                                          EMBL; U17010; AAB05846.1; EMBL; U41288; AAC49228.1;
                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                oxidoreductase; NAD; Ubiquinone; Mitochondrion SEQUENCE 641 AA; 70674 MW; 9C64C376B72E7E6
                                                             PRINTS; PR01434; NADHDHGNASE5
                                                                                pfam; pr00361; oxidored_q1; 1.
pfam; pr00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 14.5%;
Similarity 41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
          14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 1
Pred. No. 2.4;
           Score 65.5; DB 1; Length 641;
                                          9C64C376B72E7E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local

l Similarity 19; Conserv

27.9%;

Conservative

12;

Pred. No. 6.5;

Mismatches

В δÃ 밁

582 GIFARDID 589

53 GIYYRNAD 60

CHLTR

16-OCT-2001 108_CHLTR

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GUB_CLOTM STANDARD; PKI; JJT (...
P29716; p37074;
01-APR-1993 (Rel. 25, Created)
01-JUN-1994 (Rel. 25, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    148 SQLSAYYQTPVLAKALGGKKRVSSAAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001284; AAC67699.1; -. PHCI-2DPAGE; O84110; -.
                                                                                                                                                                                                                                                                                                                                                                   55 -----YYRNADIC----SRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                              91 NIQLIAYHLPL---DAHTTIGNNWKVARDLGWEQLESFGSSQPSLGVKGVFPEMEVHDFI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aramitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SLOLILLLIPSISHEAHKTSLSSWK--HDQDWANVSNWTFSNGKLRVKGI------ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE UPFOL35 (NIF3) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 SLLGISLALIVLKDPKKMHSIEKPEGLLNTVNITRWLSSKSYWFDNVYNTVLISGSLHFG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eete proteome.
ENCE 251 AA; 27474 MW; A4C2F6BE7517298E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AILTLSLOLILLLIPSISHEAHK-----TSLSSWKHDODW--ANVSNMTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01784; DUF34; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1a trachomatis.";
282:754-759(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR00486; DUF34; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%;
26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1; Length 251; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aravind L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                         PERMANARA PARARA PARARA
                                                                                 ACT_SITE
ACT_SITE
                                                      DOMAIN
                                                                                                                                                                            Pfam; PF00404; Dockerin 1; 2.
Pfam; PF00722; Glyco_hydro_16; 1.
PRLNTS: PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PROSITE; PS01034; EF_HAND; UNKNOWN_2.
PROSITE; PS00448; CLOS_CELLULOSOME_RPT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S23498; S23498
PIR; JS0611; JS0611
PIR; S18726; S18726
HSSP; P23904; LAJK
                                       DOMAIN
                                                                                                                                                          SIGNAL
                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                               HSSP; P23904; LAW.
InterPro; IPR002105; Dockerin_1.
InterPro; IPR002048; EF-hand.
InterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zverlov v.v. Velikodvorskaja G.A.;

"Cloning the Clostridium thermocellum thermostable laminarinase gene in Escherichia coli; the properties of the enzyme thus produced.";

In Escherichia coli; the properties of the enzyme thus produced.";

In Escherichia Crivity: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

In Subunii: May form Part of A MILIENZYME COMPLEX (CELLULOSOME).

WELL AS IN OTHER C.THERMOCELLUM CELLULOSOME ENZYMES. THIS ENZYME AS ANY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.

II SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X63355; CAA44959.1; -. EMBL; X58392; CAA41281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zverlov V.V., Laptev D.A., Tishkov V.I., Velikodvorskaja G.A.; "Nucleotide sequence of the Clostridium thermocellum laminarinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zverlov V.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 181:507-512(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 27405 / DSM 1237;
MEDINE-92155194; PubMed-1740123;
Schimming S., Schwarz W.H., Staudenbauer W.L.;
"Structure of the Clostridium thermocellum gene licB and the encoclethenases joined to the reiterated domain of clostridial cellulases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92095946; PubMed=1755832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 204:13-19(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) (Laminarinase).
LICB OR LAM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1515;
                                                                                                                                                                       Glycosidase;
                                  28
136
140
252
273
                            334
136
140
269
331
                                                                                                                                                             Signal; Repeat.
BETA-GLUCANASE.

NUCLEOPHILE (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

PRO/THR-RICH (LINKER).

2 X 24 AA APPROXIMATE REPEATS.
                                                                                                                                        POTENTIAL.
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SEQUENCE FROM N.A.

NCBI_TaxID=813;

RESULT 8
GUB_CLOTM

Qy

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Matches Query Match

ocal

Similarity

TIGRFAMs;

DUF34;

interPro;

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Best Local
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                                                          Matches
                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
0rotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
(OMPDCase) (OMPdecase) (Uridine 5'-monophosphate synthase) (UMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                         Appl. Microbiol. Biotechnol. 40:361-364(1993).
-i- CATALYTIC ACTIVITY: Orotidine 5'.phosphate - UMP + CO(2).
-i- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene replacement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merckelbach A., Goedecke S., Janowicz Z.A., Hollenberg C.P.; "Cloning and sequencing of the ura3 locus of the methylotrophic yeast Hansenula polymorpha and its use for the generation of a deletion by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia angusta (Yeast) (Hansenula polymorpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRF_PICAN Q06375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PICAN
                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94128354; PubMed=7764392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4905;
                                                                                                                                  Pyrimidine biosynthesis; Lyase; Decarboxylase. ACT_SITE 92 92 BY SIMILARITY.
                                                                                                                                                                                                                           EMBL; X69461; CAA49221.1; -. PIR; S31323; S31323.
                                                                                                                    SEQUENCE
                                                                                                                                                                                Pfam;
                                                                                                                                                                  PROSITE;
                                                                                                                                                                                               InterPro; IPR001754; OMPdecase.
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                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VSNMTFSNGKL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISLLMASLLLVLSVIVAPFYKAEAATVVNTPFVAVFSNFDSSQWE-KADWANGSVFNCVW 64
DRKFADIGNTV----KLQYKGGIYRTSKWADITNAHGVTGAGI 128
                           DQDWANVSNMTFSNGKLRVKGIYYRN---ADICSRHRVTSAGL 72
                                                                                                                                                                                                              P03962; 1DQW
                                                                                                                                                                               PF00215; OMPdecase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                         Similarity
                                                                                                                                                                PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA;
                                                                                                                     263 AA;
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308
304
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ascomycota; Saccharomycotina; Saccharomycetes;
; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37897 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%;
27.8%;
                                                                                                                     29275 MW;
                                                                       14.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 1; Length 334; Pred. No. 4.6;
                                                          7;
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2.
QSVADVNRDGRIDSTDLTMLKRYLIRAIPSL ->
PODGCGRHDRYVDSGSK (IN REF. 2 AND 3)
                                                                       Score 63.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                     0934EF673B03A820 CRC64;
                                                            Mismatches
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                                                                         .9;
                                                                                       DB 1;
                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                      Usage
                                                                                       Length 263;
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YRAN_HAEIN
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                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003509; UPF0102.
Pfam; PF02021; UPF0102; 1.
TIGRFAMS; TIGR00252; TIGR00252;
Hypothetical protein; Complete F
SEQUENCE 119 AA; 13812 MW: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein HI1656 HI1656.
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                                                                                 O9XS77:
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-1 beta precursor (IL-1 beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32838; AAC23300.1; -. TIGR; HI1656; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
              Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG,
NCBI_TaxID=9337;
                                                                                                                                                                       IL1B_TRIVU
                                                                                                                                                                                                                                                            102 IAFGKTPQDIQ-W 113
                                                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                                                                                                         10 LILLLIPSISHEAHKTSLSS--WKHDQDWANVSNMTFSNGKLRVKGIYYRNADICSRHRV 67
                                                                                                                                                                                                                                                                                            68 TSAGLTLQDLQLW
                                                                                                                                                                                                                                                                                                                            IVFVEVRORSHSAYGSAIESVDWRKQQKWLDAANLWLAKQNMSLE-----DANCRFDL 101
                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 32, Last sequence update)
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                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                              80
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21.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 1; Length 119; Pred. No. 1.8;
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome.
B7359D8181F31AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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IPNS_STRCI
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Best Local
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       Streptomyces clavuligerus.

Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                 IPNS_STRCL STANDARD;
P10621;
O1-JUL-1989 (Rel. 11, Created)
O1-JUL-1989 (Rel. 11, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                                   synthase).
NCBI_TaxTD=1901;
                                                                                                                                                                                                          STRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002348; IL1_HBGF.
InterPro; IPR003502; IL1_propep.
InterPro; IPR000975; Interleukin_1.
Pfam; PF00340; IL1; 1.
Pfam; PF02394; IL1_propep; 1.
PFINTS; PR002562; IL1HBGF.
                                                                                                   Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Macrophage; Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00253; INTERLEUKIN_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00125; IL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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SEQUENCE FROM N.A.
MEDLINE-99221044; PubMed=10206203;
Wedlock D.N., Goh L.P., Parlane N.A., Buddle B.M.;
"Molecular cloning and physiological effects of brushtail possum interleukin-lbeta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                               123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01584; 1HIB
                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                     12 LLLIPSISHEAHKTSLSS-WKHDQDWANVSNMTFSNGKLRVKGIYYRNADI----CSRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Immunol. Immunopathol. 67:359-372(1999).

FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY. IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                       VMVIVAIEKMKHLNGLSSQFFQDNDLMNIFTNIFQE-----EPITFKNCDIYESDSSFRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                         VSSQDCTIQDINQKCLALSKASELRALH 150
                                                                                                                                                                                                                                                                                                          VTSAGLTLQDLQLWC-----NLRIIH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD002536; Interleukin_1; 1
                                                                                                 (Rel. 11, Last sequence update)
(Rel. 38, Last annotation update)
in N synthetase (EC 1.-.-.-) (IPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
31141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             13.5%; Score 61.5; E 27.3%; Pred. No. 6.9;
                                                                                               OH)
                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; Inflammatory response; Pyrogen BY SIMILARITY, INTERLEUKIN-1 BETA.
                                                                                                                                                                                      PRT;
                                                                                            1.-.-) (IPNS) (Isopenicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTERLEUKIN-1 BETA.
307A1FE3B627D6E7 CRC64;
                                                                                                                                                                                      329
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
                                                                                                                                                                                                                                                                                                                                                                                                               34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
     Streptomyces.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                               7_BOVIN
CYAT_BOVIN
STANDARD; PRT; 1078 AA.
Q29450; 002856;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Adenylate cyclase, type VII (EC 4.6.1.1) (ATP
(Adenylyl cyclase).
SEQUENCE FROM N.A
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                    NCBI_TaxID=9913;
                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin METAL 212 212 IRON (BY SIMILARITY) METAL 214 1RON (BY SIMILARITY) METAL 268 268 IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; A01132; CAA00131.1; -.
PIR; A29894; A29894.
HSSP; P05326; IBLZ.
Interpro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00185; IPNS_1; PROSITE; PS00186; IPNS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00682; IPNSYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005123; 20G-FeII_0xy.
InterPro; IPR002283; IPN_synth.
InterPro; IPR002057; Isopen_N_synth.
Pfam; PF03171; 20G-FeII_0xy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restructed by the European Bioinformatics institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CLORING and nucleotide sequence determination of the isopenicillin synthetase gene from Streptomyces clavuligerus."; Gene 62:187-196(1988).

-!- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS FROM DELTA-L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE (ACV) TO FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leskiw B.K., Aharonowitz Y., Mevarech M., Wolfe S., Vining L.C., Westlake D.W.S., Jensen S.E.; "Cloning and nucleotide sequence determination of the isopenicil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 PMIAAGTPMHEVNLW 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE=88212175; PubMed=3130293;
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SEQUENCE FROM N.A.
STRAIN=ATCC 27064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 IPSISHEAHKTSLSSWKHD------QDWANVSNMTFS--NGKLRVKGIYYRNADICSRH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQDVVNEFHGAMTDQEKHDLAIHAYNPDNPHVRNGYYKAVPGRKAVESFCYLNPDFGEDH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVTSAGLTLQDLQLW 80
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                                                                              Bovinae;
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214
268
329 AA;
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24.0%;
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Pred. No. 8
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                                                                                                   Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PENICILLIN AND
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                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
          NUD1_YEAST STANDARD;
P32336; Q08895;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last ann)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   791 WHLKTMTNFYLVLFYTTLIMLSRQIDYYCRL 821
                                                                                                                                                                                                                                                                                                                         739 MSLELKYVLLTVALVAYLVLFNVYPSWQWDCCGHSLGNLTGTNGTL----
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HSSP; P26769; IAB8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Voelkel H., Beitz E., Klumpp S., Schultz J.E.; "Cloning and expression of a bovine adenyly1 cyclase type VII specific to the retinal pigment epithelium."; FEBS Lett. 378:245-249(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96149441; PubMed=8557110;
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                                                                                                                                                                                                                                                                                        64
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protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE RETINAL PIGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate
                                                                                                                                                                                                                                                                                 RHRVTSAGLTL------QDLQLWCNL 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.5%;
            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120819 MW;
                                     Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61.5;
Pred. No. 34;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-S0E89BF08E37FCBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                               851 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                      GLT1_YEAST STAN
Q12680; Q12290;
01-NOV-1997 (Rel. :
01-NOV-1997 (Rel. :
30-MAY-2000 (Rel. :
                              Filetici P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P. "Sequence of the GLT1 gene from Saccharomyces cerevisiae reveals the domain structure of yeast glutamate synthase.";
                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharon
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                         Glutamate synthase [NADPH] precursor (EC 1.4.1.13) (NADPH-GOGAT). GLT1 OR YDL171C.
SEQUENCE FROM N.A.
                           Yeast 12:1359-1366(1996).
                                                                                  MEDLINE=97082505; PubMed=8923741;
                                                                                                       STRAIN-CN36
                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X62147; CAA44073.1; -. EMBL; Z75281; CAA99704.1; -. PIR; S19056; S19056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                           457
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Submitted (JUL-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                        51 -----VKGIYYRNADI-CSRHRVTSAGLTL---QDLQ 78 ::|| ::|| :| || :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: REQUIRED FOR NUCLEAR DIVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                 QLISILTSKLS-----GSPSYDSDWEKILKVDLSRGKLKNMFGMQRLLPNVLVLNLS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S0005900; NUD1.
rPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                          DNEMNTLEGIPSNVVQLFCSNNKITSAHCSLAGFHDLE 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00560; LRR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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266
5
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                                                                                                                                                                                                                                    35, Created)
35, Last sequence update)
39, Last annotation updat
                                                                                                                                                                        Ascomycota; Saccharomycotina; Saccharomycetes;
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23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61;
Pred. No.
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                                                                                                                                                                                                                                                                                                 PRT;
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CB9F0408633C1315 CRC64;
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                                                                                                                                                          Saccharomyces.
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STRAIN=S288c;

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SOLUTION OF THE TANK AND DESCRIPTION OF THE TANK AND DESCR
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Best Local Similarity
Matches 20; Conserve
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Search completed: December 8, 2002, 19:31:26 Job time: 24.2774 secs
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EMBL; Z67750; CAA91574.1; -.
EMBL; Z74219; CAA99745.1; -.
SGD; S0002330; GLT1.
InterPro; IPR002489; DUF14.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR002932; Glu_synthase.
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SEQUENCE
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; pF00070; pyr_redox; 1.
pfam; pF01493; DUF14; 1.
pfam; pF01645; Glu_synthase; 1.
proDom; pF01645; Glu_synthase; 1.
TIGRFAMS; TIGR01317; GOGAT_sm_gam; 1.
Oxidoreductase; Iron_sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutamate biosynthesis; Zymogen.
                                                                                                                                                                                                                            348 TLSLPEAVMMVPEAYHKDMDSDLKAW-YDWAACLMEPWDGPALLTFTDGRYCGAILDRN 406
                                                                                                                 407 GLRPCRYYITSDDRVICA 424
                                                                                                                                                                      53 GI----YYRNAD---ICS 63
                                                                                                                                                                                                                                                                                  5 TLSL-QLILLIPSISHEAHKTSLSSWKHD-----QDWANVSNWTFSNGK-----LRVK 52
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1131
1184
1190
1195
106
449
1752
2144
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172
451
1752
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1183
1184
1190
1195
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1184 IRON-SULFUR (3FE-4S) (BY SIMILARITY).

1190 IRON-SULFUR (3FE-4S) (BY SIMILARITY).

1195 IRON-SULFUR (3FE-4S) (BY SIMILARITY).

30 I -> D (IN REF. 2).

172 TSRRFYY -> NVPVDSTI (IN REF. 2).

451 IPS -> FLV (IN REF. 2).

1752 L -> V (IN REF. 2).

1752 L -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 61; DB 1; Length 2144; 25.6%; Pred. No. 86;
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1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	and is delived by sult Query No. Score Match I	PIR_73: 1: pir1 2: pir2 3: pir3 4: pir4 4: pir4	Post-processing: Minimum Maximum Listing	Minimum DB seg length: 0 Maximum DB seg length: 200	Searched: 283224 seqs Total number of hits satisf	LOSUM6 apop 1	Title: US-09-880- Perfect score: 455 Sequence: 1 MAILTLSL	OM protein - protein search, Run on: December 8,	Copyright
296 2 E72203 307 2 T45103 286 2 B96615 510 2 JC6516 641 2 S63645 210 2 T04933 251 2 C71557 276 2 E96990 427 2 F83984 334 1 S33323 561 2 AG2336 813 2 F83476 119 2 C64174 145 2 D97407 345 2 AE2625 638 2 T47569 329 2 A29894 1451 2 S61041 455 2 AB0534 455 2 AB0534 1101 2 T20881	SUMMARIES Length DB ID	ber of results predicted ber of results predicted bereal to the score of the total score	Match 0% Match 100% first 45 summaries	0 2000000000	ying chosen parame) , Gapext 0.5	457-4 QLILLLIPSISH	h, using sw model 8, 2002, 19:27:28; Search time 29.18 (without alignments) 286.555 Million cell	GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd.
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13.2 13.2 13.1 13.1 13.1 13.1 13.1 13.1
354 785 169 216 216 217 277 561 2391 2391 769 958
C97614 S54098 D84027 S56421 D91275 D86116 AH1710 T16845 T18645 T15023 A27409 T22256 T29796 AC1998
hypothetical 32.0K aminopeptidase (EC molybdopterin-guan probable hexulose-probable hexulose-probable hexulose-probable hexulose-probable hexulose-probable hexulose-probable hexulose-probable hexulose-probable hexulose-probable hypothetical protection protectical protec

ALIGNMENTS

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conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 21-Jul-2000
C;Date: 11-Jun-1999 *text_change 21-Jul-2000
C;Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 21-Jul-2000
C;Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 21-Jul-2000
C;Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 21-Jul-2000
C;Date: 11-Jun-1999 *text_change 21-Jul-2000
C;Date: 11-Jun-1999 *sequence_revision 11-Jun-19
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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A; Reference number: A72200; MUID:99287316; PMID:10360571
A; Accession: E72203
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A;Experimental source: strain MSB8
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1107
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A; Residues: 1-296 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T25B15,100 - Arabidopsis thaliana
hypothetical protein T25B15,100 - Arabidopsis thaliana
("Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T46103
C;Accession: T46103
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, January 2000
A;Accession: T46103
A;Accession: T46103
A;Accession: T46103
A;Accession: T46103
A;Accession: T46103
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                                                                                            A; Map position: 3
A; Introns: 63/3; 2:
A; Note: T25B15.100
                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <ALC>
A;Cross references: EMBL:AL132972
                                                                                                                                                                                                                                                       A, Experimental source: cultivar Columbia; BAC clone T25B15 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.7%; Score 67; DB 2; Length 296; Best Local Similarity 27.3%; Pred. No. 5.4; Matches 15; Conservative 11; Mismatches 19; Indels
Query Match
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                                                                                                                                                                      225/2; 267/3
                                  14.7%; Score 67;
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                                                         Length 307;
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Gene 203, 75-84, 1997
A;Title: Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a component of the A;Reference number: JC6516; MUID:98085978; PMID:9426009
A;Accession: JC6516
                                    A;Cross-references: EMBL:Z22570; NID:g473182; PID:g473183
                                                                        A; Molecule type: DNA
A; Residues: 1-310 <SAN>
                                                                                                                                                                              R;Sanchez, M.; Becker
Rome 203, 75-84, 1997
                                                                                                                                                                                                C:Species: varrowia lipolytica, Candida lipolytica
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 23-Jul-1999
C:Accession: JC6516; S44157
                                                                                                                                                                                                                                                               signal recognition particle protein Sec65 - yeast (Yarrowia lipolytica)
N.Alternate names: SRP19
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                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. Rizzo, M.; Rooney, T.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: B96615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005173; NID:g11038509; PIDN:AAG27786.1; GSPDB:GN00141
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A; Residues: 1-286 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable carbonic anhydrase T18124.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: B96615
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                                                                                                                                                                                                                                                                                                                                                                                         278 YISDREIW 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          219 CRNCEKESIKDSVMNLITYSWIRDRVKRGEVKIHGCYYNLSD-CSLEKWRLSSDKTNYGF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 AVTTLOVENIIVMGHSNCGGIAALMSHQNHQGQHSRWVMNGKAAKLRTQLASSHLSFDEQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                73 TLQDLQLW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 WAN-----VSNM-TFS-----NGKLRVKGIYYRNADICSRHR-----VTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AILTLSLQUILLLIPS-----ISHEAHKTSLSSW-----KHDQD 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AWTDDKCVLMSFDLTSEDVGVW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 HDEYKVLSFIWRHNKEWKVRSEHHVLVLGARTSWKKTQCHIHHLPVSQG-ITINGVLYYG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 ADICSRHRVTSAGLTLQDLQLW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 HEAHKTSLSSWKHDQDW--------ANVSNWTFSNGKLRVKGIYYRN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                Beckerich, J.M.; Gaillardin, C.; Dominguez, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                £4.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 66; DB; 21.1%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.38;
            Score 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 286;
Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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probable ACR - Chlamydia trachomatis (serotype D, strain UW3/Cx)
                                                                                                                                   В
                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                  A; Experimental source: cultivar Columbia; BAC clone T9A21
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-210 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T04933
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                   A; Note: T9A21.160
                                                                                                                                                                                                                                                                                                      A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:AL021713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T9A21.160 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04933
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: mitochondrion
A;Introns: 144/3; 241/3; 314/1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U41288; NID:g1236403; PIDN:AAC49228.1; PID:g1236411
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-641 <PAQ>
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J. MOl. Biol. 255, 688-701, 1996
A;Title: The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence
A;Reference number: S63635; MUID:96226032; PMID:8636971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 5 - Allomyces macrogynus mitochon C:Species: mitochondrion Allomyces macrogynus
C:Date: 19 Mar-1997 #sequence_revision 19 Mar-1997 #text_change 03-Jun-2002
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Best Local :
                                                                                               101 IPTHNLPVVGSTIDSISPSADKISIIGWGHSEDETFQSQDW-NVININYT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 41.5%; Pred. No. 7.5; Matches 17; Conservative 7; Mismatches
                                                                                                                                     3 ILTLSLQLILLLIPSISHEAHKTSLSSWKH-----DODWANVSNMTFS 45
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582 GIFARDID 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 SLÉGISÉALIVÉKDÞKKMHSIEKÞEGLLNTVNITRWLSSKSYWFDNVVNTVLISGSLHFG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 GIYYRNAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AILTLSLOLILLLIPSISHEAHK-----TSLSSWKHDQDW--ANVSNMTFSNGKLRVK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 MLTLPSI-YEAHKT-----HPKDWAN------PGRVRVQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK 52
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                                                                                                                                                                                              Conservative
                                                                                                                                                                                                      14.3%; Score 65; DB 36.0%; Pred: No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 65.5;
27.9%; Pred. No. 20;
                                                                                                                                                                           8; Mismatches 16; Indels
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                                                                                                                                                                                                                     DB 2; Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Indels
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                                                                                                                                                                               8,
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C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: C71557
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71557
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A;Cross-references: GB:AE001284; GB:AE001273; NID:g3328494; PIDN:AAC67699.1; PID:g332850
A;Experimental source: serotype D, strain UW-3/Cx
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J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable glucanotransferase (endo alpha-1,4 polygalactosaminidase related protein) [impd C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: E96990
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A;Molecule type: DNA
A;Residues: 1-276 <KUR>
                                                                                                                                                                                                                        acetylornithine deacetylase BH2678 [imported] - Bacillus halodurans (strain C-125) c;Species: Bacillus halodurans (c;Species: Bacillus halodurans (c;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002 C;Accession: F83984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE001437; PIDN:AAK78712.1; PID:915023617; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824
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                                                                             R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83984
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A; Molecule type: DNA
A; Residues: 1-427 <STO>
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                                                  A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 NWK-DESWIDVSNLKWDNYVVNTLGKNLKNKGVDGFFLDNLDVYSKYKKDSMFIGLLNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 NIQLIAYHLPL---DAHTTIGNNWKVARDLGWEQLESFGSSQPSLGVKGVFPEMEVHDFI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 ----YYRNADIC----SRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 SLQLILLIPSISHEAHKTSLSSWK--HDQDWANVSNMTFSNGKLRVKGI------ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 SWKHDQDWANVSNMTFSN-----GK-LRVKGI---YYRNADICSRHRVTSAGLTLQDL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 64.5; D
30.5%; Pred. No. 9.7;
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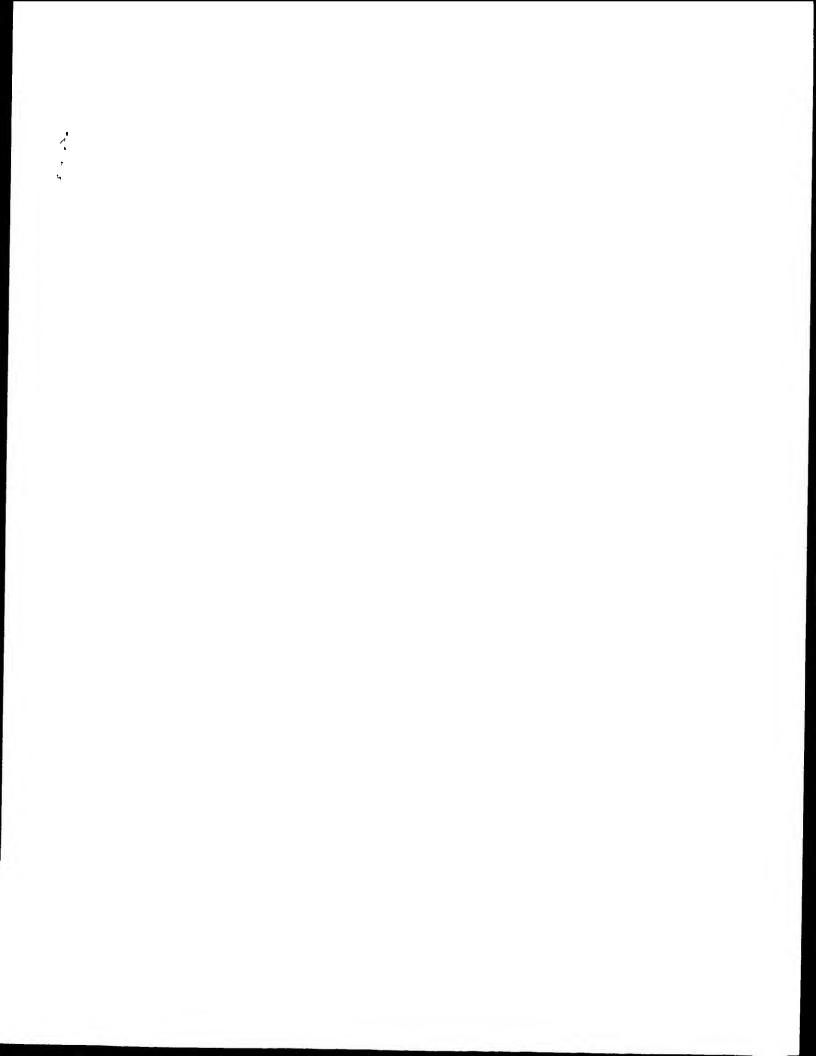
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A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06397.1; GSPDB:GA;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: BH2678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Clostridium thermocellum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: $23498; $22137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Schimming, S.; Schwarz, W.H.; Staudenbauer, W.L.
Eur. J. Biochem. 204, 13-19, 1992
A;Title: Structure of the Clostridium thermocellum gene licB and the encoded beta-1,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              licheninase (EC 3.2.1.73) licb precursor - Clostridium thermocellum N;Alternate names: beta-1,3-1,4-glucanase licB; lichenase licB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: licheninase licB; Clostridium cellulase repeat homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation E;1-27/Domain: signal sequence #status predicted <SIG> F;28-334/Product: licheninase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-334 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S23498; MUID:92155194; PMID:1740123
A;Accession: S23498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;28-334/Product: licheninase #status predicted <MAT>F;273-296/Domain: Clostridium cellulase repeat homologyF;308-331/Domain: Clostridium cellulase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X63355; NID:g40697; PIDN:CAA44959.1; PID:g40698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: licB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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                                                                                                                                                                                                                                                                                                                   orotidine-5/-phosphate decarboxylase (EC 4.1.1.23) - yeast (Pichia angusta) C;Species: Pichia angusta C;Species: Pichia angusta C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
                                                                                                                                             A; Description: Cloning and A; Reference number: S31323 A; Accession: S31323
                                                                                                                                                                                                    R;Merckelbach, A.; Goedecke, S.; Janowicz, Z.A.; Hollenberg, C.P. submitted to the EMBL Data Library, November 1992
A;Description: Cloning and sequencing of the URA3 locus of the methylotrophic yeast H
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
A;Cross-references: EMBL:X69461; NID:g2783; PIDN:CAA49221.1; PID:g2784 C;Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxy
                                                          A; Molecule type: DNA
A; Residues: 1-263 <MER>
                                                                                                                                                                                                                                                                                       C; Accession: S31323
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                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 LVQYTKTLLTF -- IYEWCHLR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RHRVTSAGLTLQDLQLWCNLR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SLQLILLIPSISHEAHKTSLSSWKHDQDW---ANVSNMTFSNGKLRVKGIYYRNADICS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 14.2%; Local Similarity 27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 KPSQVTFSNGKM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 -VSNMTFSNGKL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 14.1%; Score 64; DB 1; Length 334; Local Similarity 27.8%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 ISLLMASLLLVLSVIVAPFYKAEAATVVNTPFVAVFSNFDSSQWE-KADWANGSVFNCVW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAILTLSLQLILLLIPSISHEAHKTSL-------SSWKHDQDWAN------ 38
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Pred. No. 16
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                                                                                                                                                                     A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA1365
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                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-813 <STO>
                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83476
                                                                                                                                                                                                           A;Cross-references: GB:AE004565; GB:AE004091; NID:g9947294; PIDN:AAG04754.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                             .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable siderophore receptor PAl365 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Superfamily: H+/K+-transporting ATPase chain A
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A;Tile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A: Experimental source: strain PCC 7120 C: Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:BA000019; PIDN:BAB75945.1; PID:g17133381; GSPDB:GN00179
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A; Residues: 1-561 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Nostoc sp. (Strain PCC 7120)
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C:Accession: AG2336
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                                                                                                                            Query Match
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F;3-263/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>
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         25 TSLSSWKHÖGDWANVSNMTFSNGK-LRVKGI-----YYRNADICSRHRVT---SAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 LASLILLIHDIVVLIPSATALAYPFSLS-----GISNPSFHG----ISQVVYEYAS 461
                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 DRKFADIGNTV----KLQYKGGIYRTSKWADITNAHGVTGAGI 128
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Local Similarity 39.5%;
                                                                       Conservative
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ilarity 30.1%; Pred. No. 29;
Conservative 11; Mismatches
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                                                                                      14.0%; Score 63.5;
28.8%; Pred. No. 44;
                                                              11; Mismatches
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Pred. No. 12;
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                                                              23; Indels
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193 NAAKLVAAGMTLKDL 207
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <KUR>
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                                                                                                                                                                                                                                                                                                       A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                 A; Gene: AGR_C_701
                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE007869; PIDN:AAK86213.1; PID:g15155314; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
A;Accession: D97407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AGR_C_701 [imported] - Agrobacterium tumefaciens (strain C58, Ce C;Speckes: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: D97407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-119 <TIGR>
A;Cross-references: GB:U32838; GB:L42023; NID:g1574497; PIDN:AAC23300.1; PID:g1574505
A;Note: best homolog was a hypothetical protein from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown; translation not shown
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C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C:Accession: C64174
                                                                                                                                                                                                                                                         Query Match
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                                      144 LTMVPSFVHEL-DVSIDT----PEWGRVT-MDISYG-----GIFYALVDVRQIGLTIEKA 192
63 SRHRVTSAGLTLQDL 77
                                                                                                    12 LLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNADI-----C 62
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Search completed: December 8, 2002, 19:34:43 Job time: 37.1871 secs

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OM protein - protein search, using sw model
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1: /cgn2_6/ptodata/1/

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Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-98-362-2

US-09-052-521C-34

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Sequence 13, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence 33, Appl
Sequence 100, App
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	Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 4, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 16, Appli Sequence 3, Appli Sequence 8, Appli

RESULT 1

US-08-996-139-13 Sequence 13, Application US/08996139 Patent No. 6017729 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-996-139-13 GENERAL INFORMATION: APPLICATION NUMBER: USSN 60/06 FILING DATE: 14 CCTOBER 1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: USSN 08/81 FILING DATE: 07 MARCH 1997 PRIOR APPLICATION DATA: APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Eugene TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: TELEFAX: (200,-... ID NO: 1 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE 317 amino acids APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Euge COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6. CURRENT APPLICATION DATA: COMPUTER READABLE FORM: STREET: 51 CITY: Seattle APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430 ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street COUNTRY: CLASSIFICATION: APPLICATION NUMBER: REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER: NAME: TYPE: 98101 Perkins, Patricia Anne RATION NUMBER: 34,693 amino acid USA Floppy disk 22 DECEMBER 1997 Word for Power Macintosh 6.0.1 USSN 60/064,671 USSN 08/813,509 2851-A

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TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-995-659-13
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US-08-995-659-13
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
APPLICATION 14 OCTOBER 1997
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175 æSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNODGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                           TELEPHONE: (206)587-0430
                 15 IPSISHEAHKTSLSSWKHDQDWANVSNMTESNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
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                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                              CLASSIFICATION
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)GY: linear
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                                                                 39.7%; Score 180.5; DB 4; Length 317; 59.7%; Pred. No. 3.4e-15;
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59.7%;
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 Mismatches

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Sequence 4, Application US/09052521C Patent No. 6316408 GENERAL INFORMATION:
                                                              US-09-052-521C-4
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US-09-215-649A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                             175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                       232 ATEYLOL 238
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/996,139
FILLING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILLING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILLING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTE: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
REPLICATION DATA: US/09/215,649A
PRICATION NUMBER: US/09/215,649A
PRICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION DATA:

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappab
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                   40;
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REFERENCE/DOCKET NUMBER: 2851-A
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                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                          39.7%; Score 180.5; DB 4; Length 317; 59.7%; Pred. No. 3.4e-15;
                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                              18; Indels
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APPLICANT: Boyle, William J. TITLE OF INVENTION: Osteopro FILE REFERENCE: A-451Brv

Osteoprotegerin Binding Proteins and Receptors

CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30

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TYPE: amino acid;
TOPOLOGY: linear;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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Best Local Similarity 59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                           , MOLECULE TYPE: protein US-08-996-139-11
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APPLICANT:
                             Query Match
                 Best
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APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 IPSGS---HKVSLSSWYHDRGWAKISNMTESNGKLIVNODGFYYLYANICFRHHETSGDL 231
Matches
                                                                                                                                                              TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 ATEYLQL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 23 DECEMBER
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0
EILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                            REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
REFERENCE/DOCKET NUMBER: 20
REFERENCE/DOCKET NUMBER: 34,693
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: IMMUNICATION Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 60/
FILING DATE: 14 OCTOBER 1997
              y Match 38.7%; Local Similarity 55.4%;
                                                                                                  TOPOLOGY:
                                                                                                                                                                                               TELEPHONE:
                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Conservative
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   36;
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                                                                                                                                                                                                                                                               Perkins, Patricia Anne
                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: Apple Operating System 7.5.5 Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                294 amino acids
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunex Corporation, Law Department
                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                 (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/996,139
22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                  23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                   USSN 08/813,509
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                                                                                                                                                                                                                                        2851-A
                     Score 176; DB 3; Length 294; pred. No. 1.2e-14;
          Mismatches
                   2
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                     Gaps
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175 IPSGS---HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231

15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72

В

232 ATEYLOL 238

73 TLQDLQL 79

RESULT 5 US-09-577-780-13

Sequence 13, Application US/09577780 Patent No. 6419929 GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent Maraskovsky, Eugene

CORRESPONDENCE ADDRESS:

CITY: Seattle STATE: WA COUNTRY: USA

ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19

PRILING APPLICATION WARA.

APPLICATION UNMBER: 08/995,659

FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509

FILING DATE: <10 MARCH 1997

FILING DATE: 07 WARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: PEIKINS, PAILICIA ANDE
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEPEAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/577,780

APPLICATION NUMBER: US/09/577,780

FILING DATE: 24-May-2000
CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:

US-09-052-521C-4

Matches Query Match

Local Similarity es 40; Conserv

Conservative

39.7%; 59.7%;

Score 180.5; DB 4; Length 317; pred. No. 3.4e-15; 4; Mismatches 18; Indels 5;

5; Gaps

SEQ ID NO 4

LENGTH: 317 TYPE: PRT ORGANISM: Human

NUMBER OF SEQ ID NOS: SOFTWARE: Patentin Ve

PatentIn Ver. 2.1

40

PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1997-04-16

08/842,842

PRIOR APPLICATION NUMBER: 08/880,855 PRIOR FILING DATE: 1997-06-23

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Qγ
                                                                  В
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                                                                                                                        Matches
                                                                                                                                                Query Match
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US-08-995-659-11
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INFORMATION FOR SEQ ID NO: 11:
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211 BYLOL 215
                                           151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGEYYLYANICERHHETSGSVPT 210
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                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0.
FILING DATE: 07 MARCH 1997
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PRIOR APPLICATION DATA:
                                  75 QDLQL 79
                                                          17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                Local Similarity
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Marsskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN 60/
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/995
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple Operation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                               36; Conservative
                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                     linear
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                                                                                                                 38.7%; Score 176; DB 4; Length 294; 55.4%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apple Operating System 7.5.5 ft Word for Power Macintosh 6.0.1
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                                                                                                           Mismatches
                                                                                                      21; Indels
                                                                                                  Gaps
                                                                                                  1;
                                                                        US-09-577-780-11
                                                                                          RESULT 9
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Hest Local Similarity
Watches 36; Conserve
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US-09-215-649A-11
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GENERAL INFORMATION:
                                                                                                                                211 DYLQL 215
                                                                                                                                                         75 QDLQL 79
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Sequence 11, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEG ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09215649A Patent No. 6271349
                                                                                                                                                                                                                                                                                                        151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLKVNQDGFYYLYANICFRHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                      APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/215,649A FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
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FILING DATE: CUNKNOWN:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            38.7%;
                                                                                                                                                                                                                                                                                                                                                                                           Score 176; DB 4; Length 294; Pred. No. 1.2e-14; 6; Mismatches 21; Indels
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US-08-842-842-7
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                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08842842
Patent No. 5843678
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 11:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 DYLQL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jes 36; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 QDLQL 79
                                                                                                                                                                STREET: 1840 Dehavid
CITY: Thousand Oaks
                                                                                                                     COUNTRY:
                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
SOFTWARE:
                                                                                                      ZIP: 91230-1789
                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/577,780 FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 294 amino acids
                                                                                                                                           California
                                                                                                                                                                                    E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                         USA
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 176; DB 4; Length 294; Pred. No. 1.2e-14;
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Query Match

38.7%; Score 176;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-989-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
; MOLECULE TYPE:
US-08-989-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 7:
                                                                                                              TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: US
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                         FILING DATE: 12-DEC-
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/842,842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                           TOPOLOGY:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/032,846 FILING DATE: 13-DEC-1996
                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Conservative
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                                                         : 316 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                           linear
                    protein
                                                                                                                                                                                                                                                                                                                                   12-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jeanine D.
                                                                                                                                                                                                                                                                                                                                                    US/08/989,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 176; DB 2; Length 316; Pred. No. 1.3e-14; 6; Mismatches 21; Indels
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US-09-052-521C-34
                                                                                                                    PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 28
TYPE: PRT
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; ORGANISM: Mouse
US-09-052-521C-2
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/09052521C Patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/8
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/6
PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 08/880,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09052521C Patent No. 6316408 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 08/880,855
                                                 OTHER INFORMATION: Description of OTHER INFORMATION: Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteopro
FILE REFERENCE: A-451Brv
                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/0 PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICERHHETSGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 DYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 QDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 DYLQL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                               Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-06-23
UMBER: 08/842,842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoprotegerin Binding Proteins and Receptors
     16.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
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                                                                                                                                                                                                                 08/842,842
 Score 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 176; DB 4; Length 316; Pred. No. 1.3e-14; 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6;
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   DB
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Length
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APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: No. 6399761el Human Potassium Channels

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/09/336,643A

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR APPLICATION NUMBER: 60/116,448

PRIOR APPLICATION NUMBER: 60/116,448

PRIOR APPLICATION NUMBER: PCT/US99/03826

PRIOR APPLICATION NUMBER: DT/US99/03826

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NO5: 87

SOETWARRE: FastSEQ for Windows Version 4.0

LENGTH: 490

TYDE: PRT
                                                                             ; TYPE: PRT
; ORGANISM: H.
US-09-336-643A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-336-643A-6
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5206163-1
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                         Query Match
Best Local Similarity
             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; VIRUS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09336643A Patent No. 6399761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Miller, Andrew P. APPLICANT: Curran, Mark Edw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:|||:| :|
| 1196 MAVLTLTLLMISYVTDYFRYKRWLQCILSLIAGVFLIRSLKHLGEIETPELTIPNWR--- 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1253 -----PLTFIL-----LYLTSATVVTRWKVDIAGILLQGPQSFC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/550,816
FILING DATE: 06-JUL-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RENARD, ANDRE; DINA, DINO; MARTIAL, JOSEPH TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 DWANVSNMTFSNGKLRVKGIYYRNADICSRHRVTSAGLTLQDLQLWC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 331,037
FILING DATE: 29-MAR-1989
APPLICATION NUMBER: 752,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 14.9%; Score 68; DB Local Similarity 23.4%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-JUL-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1286
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         20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Hu, Ping
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     Conservative
                                                                                                 sapiens
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                                    DB 4;
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                                    Length 490;
   Indels 25;
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Searc Job t	Db	Qy	ф
Search completed: December 8, 2002, 19:35:31 Job time : 20.5226 secs	Db 375DTHPVTLAGKLIASTCIICGILVV 398	56 YRNADICS	Db 328 LLFLSVGISIFSVLIYSVEKDDHTSSLTSIPICWWWATISHTTVGYG
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NF-kB receptor act Amino acid sequenc Human receptor act

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OM protein - protein search, using sw model
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455
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219.722 Million cell updates/sec
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A_Geneseq_1o1002:*
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Gencore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                               Score
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AAU08386
AAB67248
AAB68273
AAB08273
                                                  AAU78286
AAW83020
AAW83195
AAW83018
                                                                                                                        Human PRO protein,
Mouse FLAG-murine
Mouse FLAG-murine
Mouse FANKL. Homo
Human RANKL Homo
Human PROJ06 polyp
Human TRANCE prote
Human TRANCE prote
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                                                            Osteoclastogenesis
Osteoclastogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor alpha.
                                                                                                       20-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-220605P.
25-JUL-2000; 2000US-220607P.
25-JUL-2000; 2000US-220634P.
25-JUL-2000; 2000US-220634P.
25-JUL-2000; 2000US-220636P.
25-JUL-2000; 2000US-220636P.
25-JUL-2000; 2000US-22083P.
25-JUL-2000; 2000US-22083P.
25-JUL-2000; 2000US-220710.
26-JUL-2000; 2000WS-US20710.
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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AAE08737
AAE04425
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NF-kB receptor act
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Human TRANCE prote
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Human full-length
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Murine receptor ac
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Amino acid sequenc
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Ъ
Antibody, OPGbp; Osteopathic, FLAG-murine OPGbp(158-316); bone resorption, loss of bone mass; bone through the matter cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                     CC encoding PRO polypeptides. The sequences of the 122 PRO polynched acids composed human secreted proteins. The sequences of the 122 PRO polynched composed and secreted proteins. The PRO nucleic acids composed antagonists are useful for diagnosing tumours, colon cancer, breast impour, proteins and antagonists are useful for treating a PRO polypeptides of the PRO polypeptides are useful for diagnosing tumours, respecially lung compositions of the PRO polypeptides. The PRO polypeptides is the proliferation of or gene expression, in prostate tumour, rectal tumour or stimulating the release of tumour prostate tumour, rectal tumour or fibroblast cells. The proliferantiation of normal ating the release of tumour necrosis factor alpha from human or stimulating composed and for the proliferation of normal human blood, and in chromosome and gene mapping. The PRO be used as molecular sequences of the invention. ANU83592-AAU83713 represent human probes, and the properties of the invention of the proliferation of the problem and the problem is a sequence of the invention.
                                                                                                              Mouse FLAG-murine OPGbp[158-316].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-2001
                                                                                                                                                                                                   AAU08386 standard; Protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                           61 ICSRHRVÍSAGLTLÓDLÓLMCNLRSV 86
                                                                                                                                                                                                                                                                                            61 ICSRHRVTSAGLTLODLOLMCNLRII 86
                                                                                                                                                                                                                                                                                            1 MAILTLSLOLILLIPSISHEAHKTSLSSWKHDODMANVSNWTFSNGKLRVKGIYYRNAD 60
                                                                                                                                                                                                                                                                                                              1 MAILTLSLOLILLIPSISHBAHKTSLSSWKHDODWANVSNWTESNGKLRVKGIYYRNAD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, such as lung cancer, colon cancer, breast tumour or liver tumour. Cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2000; 2000WO-US23522.
15-SEP-2000; 2000WO-US23328.
10-NOV-2000; 2000WS-000000P.
28-NOV-2000; 2000WG-US30873.
20-DEC-2000; 2000WG-US3646.
20-DEC-2000; 2000WG-US3646.
20-DEC-2000; 2000WG-US3646.
20-DEC-2000; 2000WG-US3645.
21-EEB-2001; 2000WG-US3456.
28-FEB-2001; 2001WG-US3456.
28-FEB-2001; 2001WG-US3456.
28-FEB-2001; 2001WG-US3456.
                                                                                                                                                                                                                                                                                                                                                                                                                              84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                  96.7%; Score 440; DB 23; Length 95; Itive 1; Mismatches 1; Indels
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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RESULT 3
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Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to an antibody or antigen binding domain (or fragment, variant or derivative), which binds to an osteoprate (or cc binding protein (opsige) and which is an integen binding domain (or cc osteoclast formation or activation an antagonistic antibody or treat loss of bone mass in a managonistic antibody.

CC osteoprosis, metastasis of bone, inhibit bone resorption in a managonistic control of the correct or treat of bone, in a managonistic antibody.

CC osteoprosis, metastasis of bone, in a managonistic antibody or seepprosis, metastasis of cancer to bone mass results from treat of prevent or managonistic and to prevent or managonistic and sequence encodes FLAG-murine Opobp[158-316].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human RANKI
                                                                                                                                                                                                     18-APR-2001
                                                                                                                                                                                                                                                                AAB67248;
                                                                                                                                                                                                                                                       AAB67248 standard; protein; 152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PN
XX
PD
XX
PF
XX
PF
XX
PR
PR
PR
XX
PR
XX
PR
XX
PA
XX

                                                                                                                                                                                                                                                                                                                                                                                                                       87 EYLOL 91
                                                                                                                                                                                                                                                                                                                                                                                                           27 SIPSGSHKVTLSSWYHDRGWAKISNWYLSNGKLRVNQDGFYYLYANICFRHHETSGDLAT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SISHEAHKTSLSSWKHDODWANVSNMTFSNGKLRVK--GIYYRNADICSRHKVTSAGLTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 QDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Fig 28; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies that bind antagonistically to Osteoprotegrin binding bone, rheumatoid arthritis, hypercalcaemia of malignancy and to steoporosis, metastasis of cancer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS13369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-2000; 2000US-0511139.
22-FEB-2001; 2001US-0791153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-2001; 2001WO-US05973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200162932-A1.
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   steroid-induced osteoporosis; mutant: mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.8%; Score 181; DB 22; Length 17
56.9%; Pred. No. 8.1e-15; Length 17
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note "Note wild-type Ser-Val-Pro-Thr-Asp
substituted by Asp-Leu-Ala-Thr-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= Flag-tag
}3..87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 170;
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RESULT 4
AAB08273
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                                                                                                                                                                                                                                                                                                                       Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers.
                            12-FEB-1999;
18-NOV-1999;
                                                                                                              Homo sapiens.
                                                                                                                                AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatoid arthritis; lupus and graft versus host disease.
                                                                                                                                                                             Amino acid sequence of a human TNF ligand QPGL.
                                                                                                                                                                                                04-DEC-2000
                                                                                                                                                                                                                                  AAB08273 standard; Protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing Apo-2 ligand for increasing yield trimers, useful for therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Connell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200100832-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
          (AMGE-) AMGEN INC
                                                       11-FEB-2000; 2000WO-US03653
                                                                                            WO200047740-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2000; 2000WO-US17579
                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                  70 ATEYLOL 76
                                                                                                                                                                                                                                                                                                                                       15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                    TLQDLQL 79
                                                                                                                                                                                                                                                                                                                     IPSGS----HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 69
                                                                                                                               and graft
                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                152 AA;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pai R,
                            99US-0119906
99US-0166271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hymowitz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0141342
                                                                                                                                                                                                                                                                                                                                                                     39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shahrokh
                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kelley RF, Koumer
okh Z, Simmons L;
                                                                                                                                                                                                                                                                                                                                                                    Score 180.5; DB 2
Pred. No. 8.1e-15;
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koumenis
                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leung
                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                               AAU86148
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                     Вþ
                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
      11-MAR 1999
11-MAR 1999
11-MAY 1999
02-JUN 1999
22-JUN 1999
22-JUN 1999
26-JUL 1999
26-JUL 1999
27-JUL 1999
31-AUG 1999
                                                                                                                                                                                            cytostatic; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Fig 9; 71pp; English.
                                                                                                                      11-FEB-2000;
                                                                                                                                       26-JUL-2001
                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                           Human PRO206 polypeptide
                                                                                                                                                                                                                                                                                 AAU86148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boyle WJ,
                                                                                                                                                         WO200153486-A1
                                                                                                                                                                                                                                                              15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                 75 ATEYLQL 81
                                                                                                                                                                                                                                                                                                                                                                   73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                     2000WO-US03565
      99US-140650P.
99US-140653P.
99US-144758P.
99US-145698P.
99US-146222P.
99US-149395P.
99US-151689P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η;
                                                                        -OM66
                                                                                          99us-1
                                                                                                  99WO-US05028
                                                                                                                                                                                                                                                                                                                                                                                                                                  39.7%;
59.7%;
                                                                                -133459P.
                                                                                          [23972P
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AAB08265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 pypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins.
Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e
                                                                                                                                                                                                                                                                                                                                                                                                                    AAU86148 standard; Protein; 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180.5; DB 2
Pred. No. 8.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ن</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to
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В
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                                                                                                                                                                                                                                                                                                                            В
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                   Matches
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30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular macrophagal, stromal and blastocoelic disorders, inflammatory, immune and anglogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO
                                                                                                           Human; tumour necrosis factor-related activation induced cytokine; TRANCS; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorder.
18-AUG-2000; 2000US-226197P
                     20-AUG-2001; 2001WO-US26101.
                                                                                 Homo sapiens
                                                                                                     cartilage growth;
                                                                                                                                                                        Human TRANCE protein splice variant
                                                                                                                                                                                              18-JUN-2002
                                                                                                                                                                                                                                    AAU78286 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 61; Fig 42; 302pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH )
                                                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                      ATEYLQL 165
                                                                                                                                                                                                                                                                                                        TLQDLQL
                                                                                                                                                                                                                                                                                                                           IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 158
                                                                                                                                                                                                                                                                                                                                              IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-205567/26.
)B; ABK40274.
                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                         244 AA;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan J, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US21090.
99WO-US28313.
99WO-US28301.
99WO-US28634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A, Godow
Pan J, Pitti RM,
                                                                                                     skeletal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                                                                                                                                                           39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski PJ,
i RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                           Score 180.5; DB 2
Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney
Smith
                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
                                                                                                                                                                                                                                                                                                                                                                   18;
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                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders
                                                                                                                                                                                                                                                                                                                                                                                     244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DM;
                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glandular,
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 2
   AAW83020
                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                   Ωy
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 02-DEC-1997;
15-APR-1997;
09-JUN-1997;
                                                                                 WO9846644-A1
                                                                                                                                                                                   10-FEB-1999
                                                                                                                                                                                                                         AAW83020 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYMA-)
                                         15-APR-1998;
                                                             22-0CT-1998
                                                                                                   Homo sapiens
                                                                                                                                 osteoclast;
                                                                                                                                                                                                                                                                          159
                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                             73 TLQDLQL
                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                          ATEYLOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-304119/34.
DB; ABK12877.
                                                                                                                                                                                                                                                                                                                                                        40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                244 AA;
                                                                                                                                bone absorption
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                              79
 97JP-0332241.
97JP-0097808.
97JP-0151434.
                                         98WO-JP01728
                                                                                                                                                                                                                                                                                                                                                                39.7%;
59.7%;
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resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyted differentiation. The present amino acid sequence represents the human TRANCE protein, splice variant 2 of the invention. TRANCE is a member of the tumour necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE)-modulating agent. The method is useful for treating a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal
                                            Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                        Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilages are skeletal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPSGS----HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV MASSACHUSETTS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                    246
    factor; bone disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 180.5; DB 2
Pred. No. 1.5e-14;
4; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ن.
د.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW83195
                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic nurrocan.
 30-MAR-1998;
16-APR-1997;
                                                                                                                           Homo sapiens
                                                                                                                                                                      hypercalcaemia;
                                                                                                                                                                                   Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                                                           Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                                                                                                                                                                          11-FEB-1999
                                                                                                                                                                                                                                                                                                                AAW83195 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an osteoclastogenesis inhibitory fact (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 28; Pages 119-120; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-1997;
21-AUG-1997;
                                          15-APR-1998;
                                                                      22-OCT-1998
                                                                                                                                                         Paget's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SNOW ) SNOW BRAND MILK PROD CO
                                                                                                                                                                                                                                                                                                                                                                                      161 ATEYLQL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                         IPSGS----HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Higashio K,
a N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0217897.
97JP-0224803.
98US-0052521
97US-0842842
                                          98WO-US07584
                                                                                                                                                                      osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinosaki M,
Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 180.5; DB 1
Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomoyasu
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽, ₹
                                                                                                                                                                      activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morinaga
Tsuda E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
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RESULT 9
AAW83018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection of ord binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding oPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcamenia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for
                                                                                                                                                                                                       Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                      Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1997;
                              15-APR-1998;
                                                                22-OCT-1998
                                                                                                 W09846644-A1
                                                                                                                                   Homo sapiens
                                                                                                                                                                                     osteoclast;
                                                                                                                                                                                                                                                                                                                                            AAW83018 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-594578/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN
                                                                                                                                                                                                                                                                            10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                   232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                       bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                              98WO-JP01728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97us-0880855.
                                                                                                                                                                                     absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                              Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.7%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180.5; DB 1
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
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02-DEC-1997;

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AAW69957
ID AAW69957
AC AAW69

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (gOBM) which is a shorter chain. OBM may be used for screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as components of drugs.
14-OCT-1997;
                                             22-DEC-1997;
                                                                                  02-JUL-1998.
                                                                                                                        W09828426-A2
                                                                                                                                                                                                             RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                          NF-kB receptor
                                                                                                                                                                                                                                                                                                                 08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                       AAW69957;
                                                                                                                                                                                                                                                                                                                                                                                      AAW69957 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 36; Pages 113-114; 151pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tor, e.g. treatmen calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-594563/50.
N-PSDB; AAV69887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                                           sapiens
                                                                                                                                                                                                 RANK ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNOW BRAND MILK PROD CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higashio K,
N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamaguchi
                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
                                                                                                                                                                                                                                                                          activator RANK ligand
       97US-0064671
                                             97WO-US23775
                                                                                                                                                                                                 tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.78;
59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinosaki M,
Takahashi K,
i K, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.5; DB 1
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kobayashi
(, Tomoyasu
Yasuda H;
                                                                                                                                                                                                                                                                          (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Þ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morinaga
Tsuda E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ن</u>
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                                         02-JUL-1998.
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   22-DEC-1997;
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allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB) polypeptide. RANK is a member of the tunour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds tRANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their
                                                                                                                               RANK; necrosis factor-kappa B; NF-kB; receptor activator; immune response; inflammatory response; toxic shock; seps: RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                   NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                        08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW68293 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TMF-alpha. The products can also be used for detection and drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
07-MAR-1997;
WO9828424-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
40; Conserv
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97US-0813509
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59.7%;
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Pred. No. 2.1
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97WO-US23866.

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RESULT 12
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Best Local :
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK with a soluble composition may also be used for regulating an immune or inflammatory response, inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for alsease characterised by neoplastic cells that express RANK. The products
                Region
                                                Domain
                                                                                                                           Homo sapiens
                                                                                                                                                                   tumour necrosis factor receptor; type II transmembrane protein;
osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                     Osteoprotegerin ligand; OPGL; osteoprotegerin;
                                                                                                                                                                                                                                  Amino acid sequence of a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                  25-JUL-2000
                                                                                                                                                                                                                                                                                                                            AAY84417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
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                                                                                                                                                        response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 AA;
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                                                                                                                                                                                                                                                                (first entry)
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96US-0059978.
97US-0813509.
                                                                             Location/Qualifiers 49..69
                 /note= "extracellular stalk domain"
158..317
                                                70..157
                                                             /note=
                                                                                                                                                        osteoporosis; bone resorption
                                                                                                                                                                                                                                                                                                                            Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%;
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                                                             "transmembrane region"
"active ligand moiety"
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180.5; DB 1
No. 2.1e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                   osteoclastogenesis;
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                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                      AAE08738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                        Human; receptor activator of nuclear factor kappaB ligand; RANKL; NI tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                                                                                                        Human receptor activator of NF kappaB ligand (RANKL) protein.
                                                                                                                                                                                                                                                                                       AAE08738 standard; Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                               US6271349-B1
                                                             Homo sapiens.
                                                                                             anti-apoptotic
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                                                                                                                                                                                                                                                                                                                                                                      232 ATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                    73 TLQDLQL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    down-regulation of osteoprotegerin ligand (OPGL) activity used t, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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98US-0102896
                                                                                           signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.7%;
59.7%;
                                                                                           therapy; immunosuppressant; anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 180.5; DB 2
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CC are useful for regulating immune response and in screening for inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing cassays for inhibitors of signal transduction, e.g. for screening for inhibitors of molecules that inhibit interaction of RANK with TRAFI, TRAF2, TRAF3, CC are useful in ameliorating the negative effects of an inflammatory cresponse that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic casponse that result from triggering of RANK, e.g. in treating toxic reactions and the effects of bone resorption. RANK acts as an anticorputor signal and rescue the cells that express RANK from apoptosis. Screening tests for agonists or antagonists of RANK activity, as creening tests for agonists or antagonists of RANK activity, as careuseful of a signal via RANK. RANK composition, or to inhibit capress rank. Compounds that interfere with RANK/TRAF6 interactions are used in the capress RANK. Compounds that interfere with RANK/TRAF6 interactions care useful for modulating osteoclast function and activities. They care used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful in preparing kits for the detection of soluble RANK, or compounds that for the detection of soluble RANK, or compounds that for the detection of soluble RANK, or compounds the formation from the prosence or distribution of the detection of soluble RANK, or compounds the formation for soluble RANK, or compounds the formation of soluble RANK, or compounds the formation from the detection of soluble RANK is and constant process or compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses novel receptor activator of nuclear factor (NF)-
kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
of the tumour necrosis factor (TNF) receptor superfamily and associates
with TNF receptor associated factor (TRAF) 2 and 3 which are important
in the regulation of immune and inflammatory response. The receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that express RANK
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               (RANKL) protein from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 15; Column 71-72; 47pp; English.
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07-MAR-1997;
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                                                                                               232 ATEYLOL 238
                                                                                                                                                                                                                 15 IPSISHEAHKTSLSSWKHDQDWANVSNWTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                                                                                                                            73 TLQDLQL
                                                                                                                                                                                        IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-520313/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0064671.
96US-0772330.
97US-0813509.
97US-0996139.
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                                                                                                                                                                                                                                                                                                            39.7%;
                                                                                                                                                                                                                                                                                   Score 180.5;
Pred. No. 2.1e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                      18;
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Best Local
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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
                                                                  AAE01993 standard; Protein; 317
                   AAE01993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi | receptor activator of NF-chi B (RANK) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-407216/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human receptor activator of NF-chi B ligand (huRANKL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE04426 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                   175
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                                                                                                                                                                                                                                  73 TLQDLQL 79
                                                                                                                                                                                                                                                                            IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 AA;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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97US-0077181.
97US-0064671.
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59.7%;
                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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Pred. No. 2.1e-14;
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175

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AAE04426 RESULT 14

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                                                                                                                                                             Matches
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                            The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The present amino acid sequence is full-length human RANKL (hurankl) protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 76-77; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-329222/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999; 99US-0442029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human full-length RANKL (receptor activator of NF-kappaB ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001 (first entry)
                                                                              175
232 ATEYLOL 238
                                                                                                  15 IPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVK--GIYYRNADICSRHRVTSAGL 72
                                        73 TLQDLQL 79
                                                                                                                                                                                   Local Similarity
                                                                                                                                                             40;
                                                                            IPSGS---HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
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                                                                                                                                                                                 39.7%;
59.7%;
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Pred. No. 2.1e-14;
4; Mismatches 18
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Search completed: December Job time: 56.2613 secs

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Maximum DB seq length: 200000000
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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204
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Copyright (c) 1993 - 2002 Compugen Ltd.
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94167 53094	E782157 60	18817 A	20873 A	35750 AG	10001	0.0	1903	474	8488	2230	76170	BC768911 602743403	1330	1000/	2000	BI260179 6029/0221	5901	50046	AW750034 PM2-BT054	88893	13728	6022	0 A A A A A	AQ523546 HS_320/_A	5504	33775	F930674	Z724950 RPCI-24-	Q050697 AGENCOUR	50754 Tetrac	H671765 BOMKY36	W/50032 PM2 B103	TOOS DWS-BTO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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659 bp DNA linear GSS 03-NOV-200 pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 200-201, Fax: 1.45-503-9170, URL: hhttp://hgp.gsc.riken.go.jp/, (E-mail:chimpbes@gsc.riken.go.jp, URL: hhttp://hgp.gsc.riken.go.jp/, (E-mail:chimpbes@gsc.riken.go.jp), URL: hhttp://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL: hhttp://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL: hhttp://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL: hhttp://hgp.gsc.riken.go.jp/, CE-mail:chimpbes@gsc.riken.go.jp/, URL: hhttp://hgp.gsc.riken.go.jp/, URL: http://hgp.gsc.riken.go.jp/, URL: http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112609.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                          Seq primer: T7
Class: BAC ends.
                                                                            Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end Plate: 186 row: C column: 1
                                                                                                                                                                                                      9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org
                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_GSSs: CH230-186C1.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                    ',S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., (P. and Fraser,C.M.
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R.Site 2
/organism="Rattus norvegicus"
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                             Location/Qualifiers
1. .612
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/clone_llb="PTB Chimpanzee Male BAC Library"
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/db_xref="taxon:9598"
/clone="pm8-112609.F"
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                                                                                                                                                                                                                                                          Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                          Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,M., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                               This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                        hanzg@chgc.sh.cn
                            XhoI"
                                                         /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                        /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                        /clone_lib="GLC"
                                                                                                                                          /clone="GLCDHB01"
                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:10116"
/clone="CH230-186C1"
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        80 c
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71.3%; Pred. No. 1.6e-18;
  78 g
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Query Match

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana T-DNA flanking sequence GK-079D11-011917, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MCL19. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mgg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strizhov, N., Li,Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Weisshaar,B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosso, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for flanking sequence tag based reverse genetics
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                    Similarity
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  Conservative
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                                                                                                         D
                                                                                                                                             /note-TCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAc161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                         removed"
a 37 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strizhov, N., Li, Y. and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/clone="GK-079D11-011917"
                                                                                                                                                                                                                                                                                                                                                                                      /strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                    Score 33.8; DB Pred. No. 0.64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, M.D., Kerlawage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzegrald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gehm, C.L., Hanna, M.C., Hedblom, E., Hihkle, P. S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., He, M., J.S., Greene, J.M., Gruber, J., Huston, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                    11 ATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGGCAAACGTCTCCAACATGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
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                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                  /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
|note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                               /db_xref="ATCC (inhost):156679"
                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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54.3%;
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 Mismatches

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                                                                                                          490 CCAGAAAGACATACATGGATGGTATGCACTCATTGATAAGTGGCTATTAGCCCCAAATGCT 549
                                               550 TGAATTACTCTAGA 563
                                                                    122 ACATTTGCTCTCGA 135
                                                                                                                                                                                62 CCAACATGACTTTCAGCAACGGAAAGTTAAGAGTCAAAGGCATTTATTATCGGGAATGCCG 121
                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 99 row: C column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., of Jong,P. and Fraser,C.M.
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Mammalia; Eutheria; Rodentia;
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CH230-99C2, DNA sequence.
BH314331
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                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong" 177 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Organism="Rattus norvegicus"
/Strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-99C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                               16.3%;
53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         type="Brain"
                                                                                                                                                                                                                                                      Score 33.2; DB 17; Length 853; Pred. No. 1.8; 0; Mismatches 63; Indels 0
                                                                                                                                                                                                                                                                                                                                                   184 g
                                                                                                                                                                                                                                                                                                                                                     177 t
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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AV979271
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KEYWORDS
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                                                                  DEFINITION
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AW750032
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                                                                                                                                                                              318
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         AV979271
AV979271.1 GI:19468995
                                                                                                                                                                                                                                                                                                                      64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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AW750032.1
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/clone_lib="BT0546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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258 AAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTGAAGGCACGA 317
                                                                                                                                                                                                                                                                                                     71 CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCCAAACGTCTCCCAACATGA 70
                                                                                                                                                                                                                                         ATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAGACATT 373
AV979271
AV979271 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg52120 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-BT0546-
120100-001-a08&t3=2000-01-12&t4-1)
Seg primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW750032 407 bp mRNA linear EST 28-APR-200 PM2-BT0546-120100-001-a08 BT0546 Homo sapiens cDNA, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: breast; Vector: pucl8; Site_1: SmaI, Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32.8; DF Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 TCAAACCAGCACCTGCGTTGGTTAAACTCAAGAAACTTGAGAAATCGGCACCACTGGGAC 287
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Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 561)

Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                           Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH671765 724 bp DNA linear GSS 19-FEB-2002
BOMKY36TR BO_2_3_KB Brassica oleracea genomic clone BOMKY36, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH671765.1 GI:18736884
                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
                                                       Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                 Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                         Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                           Contact: Chris Town
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                                                                                                                                           301-838-0208
                                                                                                                                                                                   Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                             301-838-3523
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                                                                                                 from a doubled haploid provided by
                                                                                                                         cdtown@tigr.org
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127 c 127 g 157 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
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                                 Location/Qualifiers
/organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodontidae; Tetraodon.

1 (bases 1 to 823)

Roest Crollius, B., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Saurin, W. and Weissenbach, W. and W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            004K23 of library B from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roest-Crollius,H., Jaillon,O., Dasilva,G., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL350754.1 GI:8244524
                                                                                                                                                                                                                                                                                                          This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                       185
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/rote="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" a 144 c 162 g 192 t
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/clone="BOMKY36"
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                                                                                                                       /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="004K23"
/clone_lib="B"
/note="Genoscope sequence ID : COABOO4AF12B1-end : SP6"
/note="Genoscope sequence ID : COABOO4AF12B1-end : SP6"
154 c 189 g 259 t 36 others
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Pred. No. 2.3;
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BASE COUNT
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BQ050697/c
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TITLE
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                                             129 CTC 131
                                                                  628 TTTTTTTTAGTTTGGAAAAGTAAATCTGAAAGAAGTAAATTCATTTAATCAATACATCAG 569
                                                                                                                                 688 TCAAAAATAAAGTTTTATTTTTGTAAAAACTGTATAACTTTGGAACAAAGTNTAAAACAA 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                69 GACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTG 128
                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 CTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATT 190
                                                                                                                                                                 9 TCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACAT 68
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            EC 566
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                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT_6808690 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784700 BQ050697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                        /tissue_type="lefomyosarcoma"
/tissue_type="lefomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SpORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
233 c 214 g 292 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:5784700"
/clone_lib="NIH_MGC_71"
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1. .1027
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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53.7%;
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50.4%;
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ORGANISM
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AZ724950
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                                                                         319 AGTGCAGGCCTTA 331
                                                                                                         148 TCAGCAGGCCTAA 160
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                                                                                                                                                                                                                                                                                             Local Similarity
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Class: BAC ends.
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259 ATCCAAATCAATAACGCTTATGATCAAAAGAGAGCCATTATATAAAAATATTCAGGAAATC
                                                                                                                                                                                                                                                                                                                              199 TTTTGTAAAGATAAAGAAGATTGAACAATCCTCAGCCAAACTAATCAAGGGAAAGAGAAG 258
                                                                                                                                                                                                                                                                           88 CTAAGAGTCAAAGGCATTTATTACCGGAATGCCGGACATTTGCTCTCGACATCGCGTAACC 147
                                                                                                                                                                                                                                                                                                                                                                              28 TCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 64 row: B column: 19
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Other_GSSs: RPCI-24-64B19.TV
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Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-64B19"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Cell_type="Spleen/Brain"
/Cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/POCI-24 Mouse BAC Library produced by Pieter de Jong. The
Library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BamH1 sites using MboI partially digested male C57BL/6J
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                                                                                                                                                                                                                                                                                                                                                                    CACGAGAGTGAACAGCAGAAAGAGGCTTCTTGGAAACATAACCAGGAATGCGAAAAGCCT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-NT0135-
131200-014-g01&t3=2000-12-13&t4=1)
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Ludwig Institute for Cancer Research
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                      Homo sapiens
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                                                                                                        mRNA sequence.
BF683775
                                                                                                                                                602140058F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: nervous_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
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56.7%;
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131 CTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGA 170
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plate: LLCM1161 row: c column: 16
High quality sequence stop: 720.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                             Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishi,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU226504 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-39-G24 3',
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                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 428)
                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Large scale analysis of Arabidopsis full-length cDNP
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Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: uterus; Vector: pOTB7; Site_1: XhOI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library.
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/clone_lib="NIH_MGC_46"
/tissue_type="leiomyosarcoma_cell_line"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 4.8;
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Search completed: December Job time: 459.782 secs
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Best Local Similarity
Matches 63; Conserv
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                                                                             76 CAGAAGAGAATATCTCAGAGTTTAAGGAAATATTAACTCATTTACGATTGTTC 130
                                                                                                      75 CAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCCGACATTTGC 129
                                                                                                                                                                            16
                                                                                                                                                                                              15 AACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTT 74
                                                                                                                                                                   Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                         15.6%;
ilarity 54.8%;
Conservative
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/db_xref="taxon:3702"
/clone="RAFL14-39-G24"
/clone_lib="RAFL14"
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="root"
/lab_host="bH10B"
/note="Site_1: BamHI; Site_2: SalI"
/note="Site_1: BamHI; Site_2: SalI"
92 c 73 g 123 t
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                    8, 2002, 19:27:16
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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400769
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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    1186
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7908.746 Million cell updates/sec
                                NF-kB receptor act
NF-kB receptor act
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Human receptor act
Human full-length
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                                                                                                                                                    cDNA encoding huma
Nucleic acid encod
Nucleic acid encod
                   CDNA encoding huma
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RESULT 1 ABK33576 standard; cDNA; 1186 BP. AC ABK33576; XX ABK33576; XX ABK33576; XX CDNA encoding human PRO protein, Seq ID No 81. EX CDNA encoding human PRO protein, Seq ID No 81. XX Human; secreted protein; PRO; tumour; lung cance, breast cancer; prostate tumour; rectal tumour; 1 KW POTICITY COLOR PRO; tumour secretal protein, seq ID No 81. XX COS HOMO Sapiens. XX PN WO200208288-A2. XX 29-JUN-2000; 2000US-21066. PR 25-JUL-2000; 2000US-210664P. PR 25-JUL-2000; 2000US-220634P. PR 25-JUL-2000; 200US-220634P. PR 25-JUL-2000; 200US-22063	11 96.4 47.3 2271 1 AAZY9Y54 13 96.4 47.3 2271 2 AAYY0285 14 93.2 45.7 1823 20 AAY80223 14 93.2 45.7 1823 20 AAY80223 15 80.8 39.6 951 21 AAY69990 17 80.8 39.6 951 21 AAX99965 18 80.8 39.6 951 21 AAX99965 20 80.8 39.6 1530 19 AAY49387 21 80.8 39.6 1630 12 AAY41377 22 80.8 39.6 1630 22 AAD5526 23 80.8 39.6 1630 22 AAD5527 24 80.8 39.6 1630 22 AAD5591 25 80.8 39.6 1630 22 AAD5591 26 80.8 39.6 2029 21 AAX99955 27 80.8 39.6 2237 24 AAX92288 28 80.8 39.6 2237 24 AAX12880 39 80.8 39.6 2237 24 AAX12880 30 80.8 39.6 2237 24 AAX12880 31 80.8 39.6 2237 24 AAX12880 31 80.8 39.6 2237 24 AAX12880 31 80.8 39.6 2237 24 AAX129976 32 80.8 39.6 2237 24 AAX129971 39 61.8 30.3 519 21 AAX29971 39 61.8 30.3 519 21 AAX29971 39 61.8 30.3 546 21 AAX29977 40 61.8 30.3 546 21 AAX29977 40 61.8 30.3 554 21 AAX29977 41 31.2 15.3 493 20 AAX872947 42 31.2 15.3 3073 24 ABK46139 45 31.2 15.3 3073 24 ABK46139
81. cancer; colon cancer; pur; liver tumour; ell proliferation;	Human osteoprotege cDNA encoding huma Human TRANCE encod Rat osteoclast dif Nucleotide sequence Mucleotide sequence Mucleotide sequence Mucleotide sequence Nucleotide sequence Nucleotide sequence Nucleotide sequence Nucleotide sequence Nucleotide sequence Nucleotide sequence Nurine receptor act Murine receptor act Murine RANKL (recemouse oDM nucleotide sequence Murine TRANCE encocons DNA encoding mouse DNA encoding a syn DNA encoding a syn DNA encoding a syn DNA encoding osteo DNA encoding colo Human cytokinesis cDNA encoding colo Human cytokinesis cDNA encoding colo

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                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC The PRO polypeptides are useful for treating a PRO related disorder. CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or CC civer tumour. The PRO polypeptides are useful for stimulating the CC the proliferation of, or gene expression, in pericyte cells, for stimulating the CC the proliferation or differentiation of chondrocyte cells, for CC concern the PRO polypeptides are useful for stimulating the CC the proliferation or differentiation of chondrocyte cells, for CC concern the proliferation of chondrocyte cells, for CC concern the proliferation of chondrocyte cells, for CC concern the proliferation of comman human blood, CC concern the proliferation of comman human dermal CC concern the proliferation of comman management that the proliferation of comman management the proliferation of comman
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AAV69899;
                 AAV69899 standard; cDNA to mRNA; 741 BP.
                                                                                                 684 TGGTGTAATTTGAG 697
                                                                                                                 181 TGGTGTAATTTGAG 194
                                                                                                                                               Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;
                                                                                                                                                                                                            564 TCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCC
                                                                                                                                                                                                                                                                    504 CATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour.
                                                                                                                                                                                                                                      61 TCCAACATGACTTTCAGCAACGGAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCC 120
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                                                                                                                                                                                                                                                                                                                                                                  Local
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C, Gurney AL,
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2000US-000000P
2000WO-US30873
2000US-253646P
2000WO-US32678
2000US-0747259
2000WO-US34956
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2001WO-US34956
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2000WO-US23522.
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Smith V, Stephan JF,
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محم CK, Wood WI;
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12-AUG-1997;
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15-APR-1997;
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N, Yamaguchi K,
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                                                                                                                                  Conservative
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97JP-0151434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinosaki M, Kobu, Takahashi K, Tomoyası
                                                                                                                             0; Mismatches
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The present sequence encodes an osteoclastogenesis inhibitory factor (OCLF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone obsorption factors such as calcitriol or parathyroid hormone (PTH). The protein factor by separation and solubilisation of membrane proteins then affinity chromatography using OCLF. It exists in a full-sequence used for screening potential inhibitors and modifiers of its biological These substances can then be used in the treatment of disorders of bone of the protein, for investigative and diagnostic purposes, and as
117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;
                                                                                    378 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 437
                                                                                                                                                                                                    318 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                           63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                     3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding a human OCIF-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                  47.3%; Score 96.4; DB 19; Length 741; 74.5%; Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kobayashi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomoyasu A,
                                                                                                                                                                                                                                                                                                                          41; Indels
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Tsuda E;
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15-APR-1997;
09-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding a human OCIF-binding molecule (OBM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV69887 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoclast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9846644-A1
                                       (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). By a solubilized from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins absorption factor by separation and solubilisation of membrane proteins absorption actoring form (sobm) which is a shorter chain. OBM may be form and a solubilised form (sobm) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological used for screening for receptors to OBM which mediate its function. activity, and screening for receptors to OBM which mediate its function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                        Nakagawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                         Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1998;
                                                                                                                                                                                                                                                                                                               protein binding to osteoclastogenesis inhibitory factor - useful
                                                                                                                                                                                                                       The present sequence encodes an osteoclastogenesis inhibitory factor
                                                                                                                                                                                                                                                         Claim 38; Page 115; 151pp; Japanese
                                                                                                                                                                                                                                                                                     calcium metabolism
Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
                               of the protein, for components of drugs.
                                                                                                                                                                                                                                                                                                                                             -PSDB; AAW83018
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                                                                                                                                                                                                                                                                                                  treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone absorption factor; bone disorder; calcium metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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                                                                                                                                                                                                                                                                                                                                                                                                 Yasuda H;
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Best Local Similarity

47.3%;

Score 96.4; DB 19 Pred. No. 2.3e-23;

DB 19;

Length 954;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9828426-A2
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                                                        activator of necrosis factor kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell may be used for inhibiting activation as soluble RANK which binds to expressing membrane-associated RANK not a soluble RANK and can be RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their
                                                                                                                                                                                                                                                     New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                 Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
                                                                                                                                                                           This cDNA encodes a human RANKL, a ligand for the RANK (receptor
                                                                                                                                                                                                                     Claim 25; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW69957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Galibert LJ,
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97US-0813509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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23-DEC-1996;
07-MAR-1997;
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New isotated receptor activator of necrosis factor-kappa B - useful
                                         P-PSDB; AAW68293
                                                      WPI; 1998-377655/32.
                                                                                   Anderson DM,
                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                           22-DEC-1997;
                                                                                                                                                                                                                       02-JUL-1998.
                                                                                                                                                                                                                                              WO9828424-A2.
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                                                                                                                                                                                                                                                                                                                                                         RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                                                                                                                                                                                                                  RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
                                                                                                                                                                                                                                                                                                                                                                                                          NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease can also be used to identify inhibitors of RANK RANKL Polypeptides an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                              Galibert LJ,
                                                                                                                                 97US-0064671.
96US-0059978.
97US-0813509.
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                                                                                                                                                                                       97WO-US23866.
                                                                                                                                                                                                                                                            /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%;
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                                                                            Maraskovsky E;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3e-23;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor CC activator of necrosis factor kappab (NF-kB)) polypeptide. RANK is a CC member of the tumour necrosis factor (TNF) family. Host cells transformed CC nucleic acid can be used to produce recombinant RANK protein. The soluble CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CC used for regulating an immune or inflammatory response. Inhibition of CC Used for regulating an immune or inflammatory response. Inhibition of CC inflammatory response that result from triggering of RANK, e.g. in CC inflammatory response that result from triggering of RANK, e.g. in CC inflammatory reactions. They can also be used in adjunct therapy for can also he used to reactions or acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
            17-DEC-1998;
                                              07-AUG-2001.
                                                                                 US6271349-B1.
                                                                                                                                                                     Key
                                                                                                                                                                                                                   anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                      Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                                                                                                                                                                                                                                          Human receptor activator of NF kappaB ligand (RANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD15311 standard; cDNA; 954 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAD15311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 711 ACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 TGCCGACATTTGGTCTCGAGATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for, e.g. developing products for regulating an immune or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTATCAGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TGAGGCTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 47.3%;
Similarity 74.5%;
         98US-0215649
                                                                                                 /product= "Human RANK ligand (RANKL) protein"
                                                                                                                                                                Location/Qualifiers
                                                                                                                                /*tag=
                                                                                                                                                   ..954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
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CC Rappab (RANK) proteins and their corresponding DNAs. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates con the regulation of immune and inflammatory response. The receptors care useful for regulating immune response and in screening for inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing concludes that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, concludes that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, concludes that result from triggering of RANK, e.g. in treating toxic complex that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic consolves that result from triggering of RANK, e.g. in treating toxic consolves that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic consolves the result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic consolves the result from triggering of RANK acts as an anticonstance of the receptor are used in vivo or in vitro based consolves and the effects of bone resorption. RANK acts as an anticonsolves are used as a signal via RANK, and compositions are used in the consolves and antagonists of RANK compositions are used in the consolves and antagonists of RANK compositions are used in the consolves and for modulating the formation of osteoclast from osteoclast consolves and for modulating osteoclast function and activities. They recurred and as immunosuppression of recombinant proteins, as probes for analysis useful for the expression of recombinant proteins, while the proteins care useful in preparing kits for the detection of soluble RANK, or and the presence or distribution of RANK transcripts, while the proteins are useful consolves and activities. The proteins are consolved activity. The present sequence is a cDNA encoding monitor RANK lightly consolved activity. The present s
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07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dougall WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses novel receptor activator of nuclear factor (NF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Column 69-71; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           human RANK ligand (RANKL) protein.
                                                                                                                                                                                                                  531 TEGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCCAAGATCTC 590
                                                                                                                               591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
177
                                            651
                                                                                117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                          63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                          Match 47.3%;
Local Similarity 74.5%;
                                                                                                                                                                                                                                                          3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                        GCTA 180
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                                                                                                                                                                                                                                                                                                           Conservative
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96US-0772330.
97US-0813509.
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97US-0077181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2001
                                                                                                                                                                                                                                                                       The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAP) 2 region. RANK associates with TNF receptor-associated factor (TRAP) 2 region. RANK associates with TNF receptor-associated factor (TRAP) 2 region. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huranKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Column 61-64; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-407216/43.
                                                                                                                                                                                                                           Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                 531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                Local Similarity
                                                                63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                              3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                 Conservative
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97US-0077181.
97US-0064671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human RANKL protein"
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                                                                                                                                                                                    47.38;

 Mismatches

                                                                                                                                                                                    Score 96.4; DB 22; Length 954; pred No. 2.3e-23;
                                                                                                                                                                         Indels
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CC The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I CC factors (TRAFs). Triggering of RANK by overexpression or co-expression CC of RANK and membrane bound RANK by overexpression or co-expression CC of the transcription factor NF-kappaB, a ubiquitous transcription factor CC that is most extensively utilised in cells of the ammune system.

CC inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating cc negative effects of inflammatory reactions, and the effects of excess CC for the preparation. The RANK DNAs, proteins and their analogues are useful cc eals for use in gene therapy applications in diagnosing diseases CC may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct CC osteolysis (FEO) and early onset paget's disease of bone (FEO), The present-sequence is a cDNA encoding full-length human RANKL (hurannel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD05904
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                                                                                                                                                                                                                                                                                                                      Example 7; Page 75~76; 96pp; English.
                                                                                                                                                                                                                                                                                                                                           New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAE01993
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2000; 2000WO-US31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200136637-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human full-length RANKL (receptor activator of NF-kappaB ligand) protein"
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             WPI; 2002-304119/34
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                                                                                                 18-AUG-2000; 2000US-226197P.
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                                                                                                                                20-AUG-2001; 2001WO-US26101
                                                                                                                                                                28-FEB-2002.
                                                                                                                                                                                              WO200216551-A2
                                                                                                                                                                                                                                                                                                                                   misc_feature
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P-PSDB; AAU78286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human TRANCE protein splice variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK12877 standard; cDNA; 1945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Target region for antisense nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.38;
74.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation induced cytokine) protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splice variant 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.4; DB 22;
Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 954;
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ABK12876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or baving a disorder comprising insufficient on involves administering to skeletal growth. The method of the invention involves administering to the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE) modulating agent. The method is useful for treating a mammal (TRANCE) modulating agent insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, cranifesom from the selected from dwarfism, osteopetrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 2, of the invention. TRANCE is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other;
                                                                                                                                                                                 Human; tumour necrosis factor-related activation induced cytokine; TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte; exostosis bursata; multiple osteocartilaginous exostosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK12876 standard; cDNA; 2226 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 TEGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 465
                                                                                                                                                                                                                                                                                                               cDNA encoding human TRANCE protein splice variant 1.
                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 ACTA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 GCTA 180
                                                                                                                                                                   cartilage growth; skeletal growth; gene; ss.
                                                              misc_feature
                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 CAACATGACTITCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
141..190
      /note= "Tumour necrosis factor (ligand) superfamily, member 11 (INFSF11), target region for antisense
                                                 /*tag=
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Pred. No. 3e-23;
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AAZ99964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001; 2001WO-US26101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the mammal a tumour necrosis factor related activation induced cytokine (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, or skeletal discrepancies and bone or cartilage damage cranification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating mammal having disorder characterised by abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi Y, Odgren PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resulting from traumatic injury surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, growth are selected from acromegaly, gigantism, exostosis. The method exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytokine-modulating agent to mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAU78285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a new method of treating a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family and acts directly on cartilage-producing cells (chondrocytes).
AAZ99964 standard; DNA; 2271 BP
                                                                                                                                                                                                                                                                                                                                687 TEGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 746
                                                                                                                                                                                                           117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                     747 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 806
                                                                                                 867 ACTA 870
                                                                                                                                       177 GCTA 180
                                                                                                                                                                                                                                                                                          63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                           Match 47.3%;
Local Similarity 74.5%;
                                                                                                                                                                                                                                                                                                                                                                     3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                            TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 866
                                                                                                                                                                                                                                                                                                                                                                                                              137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157..1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid. Specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splice variant 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activation induced cytokine) protein,

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96.4; DB 24; Length 2226; pred. No. 3.2e-23;
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AAZ99964;

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Matches
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                                                                                                                                                                                                                                                                                                             protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL an immune response in the animal. The method and OPGL analogue to induce useful for treating, preventing and ameliorating osteoporosis or other animals.
                       835
                                                                                                                                                                                                                                                                         Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane
                                117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                775 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 834
                                                                                                                                   715 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-77; 110pp; English.
                                                                                                  63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-271444/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halkier T, Haaning J;
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02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEBI-) M & E BIOTECH AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                        w
                                                                                                                                                                                                                       Match 47.3%; Score 96.4; DB 21; Length 2271; Local Similarity 74.5%; Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response; osteoporosis; bone resorption; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUL-2000 (first entry)
TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 894
                                                                                                                                                     TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                      or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY84417
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0102896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 185..1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                            41;
                                                                                                                                                                                                          Indels
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Query Match

Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

47.38;

Score 96.4;

DB 19; Length 2274;

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The present sequence encodes human osteoprotegerin (OPG) binding protein. CC encoding opg binding protein are used to produce recombinant OPG binding cC encoding opg binding protein is used in binding assays to determine CC osteoprotegrin (OG) in biological samples; to screen for specific contracellular proteins); to raise Ab (useful in immunoassays for CC intracellular proteins); to raise Ab (useful in immunoassays for CC modulate binding of OPG binding protein) and to identify compounds that CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG contrasgenic animal models, while complementary sequences are used for CC sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for CC OPG binding protein, particularly soluble forms of OPG binding protein binding protein, particularly soluble forms of OPG binding protein contrasted sease, periodontal disease, osteoporosis, lossening of prostheses, as optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA
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                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1998;
16-APR-1997;
23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-594578/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW83195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-1999 (first entry)
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97US-0842842.
97US-0880855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "osteoprotegerin binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Conservative

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pred. No. 3.2e-23;
0; Mismatches 41

41; Indels

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74.5%;

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                                                                                                                                                                                                                                                             22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK40274 standard; cDNA; 2390 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; cytostatic; neuroprotective; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA encoding human PRO206 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK40274;
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153486-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          775 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895 ACTA 898
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                                                                                                                                                                                                                                                                                                 02-JUN-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                          11-MAR-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                          11-FEB-2000; 2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                 08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders
                                                                                                                                                                                            30-NOV-1999;
                                                                                                                                                                                                                               31-AUG-1999;
                                                                                                Marsters
                                                                                                           Ashkenazi AJ,
                                              P-PSDB; AAU86148.
                                                              WPI; 2002-205567/26.
                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 894
                                                                                                                                                          2000WO-US00219
                                                                                    Wood WI;
                                                                                                 Pan J,
                                                                                                             Goddard A,
                                                                                                                                                                                                         99WO-US21090
                                                                                                                                                                                                                     99US-151689P.
99WO-US20111.
                                                                                                                                                                                                                                           99US-149395P.
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                                                                                                                                                                                                                                                                                                                                                     99WO-US05028.
                                                                                                                                                                      99WO-US28634
                                                                                                                                                                                            99WO-US28313.
                                                                                                  Pitti RM,
                                                                                                              Godowski PJ,
                                                                                                 Roy MA,
                                                                                                    Gurney AL,
, Smith V,
                                                                                                     Stone DM;
                                                                                                                   Hillan KJ;
          disorders
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AAX80223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other bladders such as neuronal, glial, astrocytal, hypothalamic, glandular, disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocelic disorders, inflammatory, immune and anglogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 50; Fig 41; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1016 ACTA 1019
                                                                                                      11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
                                                                                                                                                                                                                                                                                                                                          TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         836 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTC 895
                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX80223 standard; cDNA; 1823 BP.
                                                                                                                                                                                                                                                                                                                                                                                                       Human TRANCE encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             896 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 955
                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                               17-JUN-1999.
                                                                                                                                                                                                                           WO9929865-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 GCTA 180
                                                                                                                                                               14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 47.3%;
Local Similarity 74.5%;
 P-PSDB; AAY17873
               WPI; 1999-385609/32.
                                            choi Y,
                                                                       (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TGAGGCTCATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137;
                                              Josien R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                       98US-0034099
                                                                                                                      98US-0989479.
97US-0989479.
                                                                                                                                                                   98WO-US26486
                                                                                                                                                                                                                                                                         Location/Qualifiers 1..738
                                                                                                                                                                                                                                                           /*tag=
                                                 Steinman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 41;
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Best Local
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       (UYWA-) UNIV WESTERN AUSTRALIA
                                        29-SEP-1999;
                                                                 29-SEP-2000; 2000WO-AU01202
                                                                                                                               WO200123549-A1.
                                                                                                  05-APR-2001.
                                                                                                                                                                                                                                                               Rat; osteoclast formation inducer; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                            Rat osteoclast differentiation factor, ODF, coding sequence.
                                                                                                                                                                                                                                                                                                                                29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    AAF86481;
                                                                                                                                                                                                                                                                                                                                                                                          AAF86481 standard; cDNA; 957 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes human TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to Agonists and antagonists of TRANCE, can be used to modulate immune cells and increasing or decreasing the life span of mature dendritic are especially useful for treating immune system related conditions such The TRANCE, autoimmune disease or hypersensitivity to an allergen. dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 ACTA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 TGCCAACATTTGGTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF like proteins for treating autoimmunity and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 CAACATGACCTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTATCAGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TGAGGCTCATAAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTGGGGTAAGATCTC 374
                                                                                                                                                                                                                                                     Differentiation Factor; bone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                     99AU-0003147.
                                                                                                                                                        /product= "Rat ODF"
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.7%;
73.4%;
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Search completed: December Job time: 65.0886 secs
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                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the coding sequence for rat Osteoclast Differentiation Factor (ODF) ODF is thought to be directly involved in Osteoclasts promote dissolution of the bone matrix and solubilisation of bone salts. The present sequence is useful in gene therapy, and as activity of cells, e.g., cell proliferation, cell differentiation and as vaccines. Anti-rat ODF antibodies are useful in assay methods for
                                                                                                                                                                                                                                                                                                                                            Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;
                                                         659 ACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACTATCTTCAGCT 716
                                                                                           122 ACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT 179
                                                                                                                              599 TGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCA 658
                                                                                                                                                                                                  539 CCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCAAGATCTCTAACA 598
                                                                                                                                                                                                                                                                                                                                                                                   quantifying ODF polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation, cell differentiation and cell viability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB82092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu J,
                                                                                                                                                              68 TGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATGCCG 121
                                                                                                                                                                                                                                   8 CTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-335526/35.
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zheng M;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                       41.2%; Score 84; DB 22; Length 957; 71.3%; Pred. No. 4.9e-19;
                  8, 2002, 17:26:22

 Mismatches

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

December 8, 2002, 16:41:40; Search time 436.856 Seconds

(without alignments)
13590.225 Million cell updates/sec

Run on:

Title:

US-09-880-457-1_COPY_543_746 204

1 catgaggctcataaaacgag.....gtaatttgagaatcattcac 204

Scoring table: Sequence: perfect score:

Gapop 10.0 , Gapext 1.0

2054640 segs, 14551402878 residues

4109280

IDENTITY_NUC

Searched:

Database :

GenEmbl:*

gb_ov:* gb_htg:* gb_ba:*

gb_pr: gb_pl:* gb_pat:*

gb_sts:* gb_ro:*

9: 10: 11: 12: 13: 14: 15: 16: 17:

em_ba:*

em_in:*

em_or:* em_om:* em_mu:* em_hum: * em_fun:*

18: 19: 20: 21: 21: 23: 23: 24: 25: 26: 27: 27: 28: 29: 30:

em_ph:* em_pl:* em_ov:*

em_ro:*

em_htg_inv:* em_vi:* em_un:* em_sts:*

em_htg_pln:* em_htg_rod:* em_htg_mus:* em_htg_other:* em_htg_hum: * em_pat:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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em_htgo_hum:* em_htgo_mus:* em_htg_vrt:* em_htg_mam:*

REFERENCE

AUTHORS

Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.

em_htgo_other:*

Result a O იი RESULT 1 AX358828 DEFINITION ACCESSION No. a ၀ ၀ SOURCE KEYWORDS VERSION Locus ORGANISM Score 96.4 96.4 96.4 96.4 96.4 96.4 96.4 96.2 80.88 80.88 80.88 80.88 80.88 80.88 80.88 80.88 80.88 80.88 79.2 35.4 35 35 35 35 1186 bp Sequence 81 from Patent W00193983. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AX358828.1 GI:18675315 Match Length DB 95.1 95.1 95.1 95.1 47.3 47.3 47.3 2390 47.2 113451 47.2 200724 39.6 276831 522 17.4 140545 17.2 175695 17.2 178631 16.6 151734 1186 165707 190748 1823 957 127812 1034 1630 1630 1630 972 1694 10 2 10 10 10 AX358828 AX362321 10 AB037599 AR156434 AB064269 AF019047 AC094149 AR164148 AB064268 AC104794 AF013173 AB064270 AX451895 AR062119 AF053713 AX201362 AX147989 E34349 AR156433 E36388 E34350 AB032772 AX140162 AR164147 AX451897 AX147987 AB032771 AR157058 AC126690 AB036798 SUMMARIES AC021225 AL606844 AF019048 AB022036S4 ALIGNMENTS DNA AB064268 Homo sapi AB061227 Homo sapi AB037599 Homo sapi linear E34350 DNA and pro E36388 Novel prote AB008426 Mus muscu AB036798 Mus muscu Description AR156433 Sequence AR164147 Sequence AX147987 Sequence AX451897 Sequence E34349 DNA and pro AB022039 Mus muscu AX358828 Sequence AC010969 Homo sapi AC104794 Homo sapi AX362321 Sequence AB064270 AX451895 AC126690 Mus muscu AX32589 Sequence AC010719 Homo sapi AL606644 Homo sapi AL512635 Human DNA AF013171 Homo sapi AF187319 Rattus no AF053712 Homo sapi AB064269 AC094149 Rattus no AF019047 AL139382 Human DNA AB032772 Mus muscu AB032771 Mus muscu AR157058 Sequence AX140162 Sequence AF062119 Sequence AF053713 Mus muscu AC021225 Homo sapi AF019048 Mus muscu AF013170 Mus muscu PAT 13-FEB-2002 Sequence Sequence Homo Homo sapi Sequence Homo sapi Homo sapi Sequence

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               624 GACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTA 683
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100.0%; Pred No. 3.8e-53;
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Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162662 bases at least Q40
Consensus quality: 163189 bases at least Q30
Consensus quality: 164786 bases at least Q30
Insert size: 9479; agarose-fp
Ouality coverage: 10.795; sum-of-contigs
Quality coverage: 10.73 in Q20 bases; sum-of-contigs
Quality coverage: 10.53 in Q20 bases; sum-of-contigs
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Sequencing vector: M13; 0%
Chamiature vector: D13; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-Apr-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 002 this sequence version replaced gi:19339129.
                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                           be preserved.
                                                                                                             as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. .165707
        Location/Qualifiers
            1112: contig of 1112 bp in length
1212: gap of unknown length
76227: contig of 75015 bp in length
76327: gap of unknown length
165707: contig of 89380 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC010969.11 GI:13677120
                                                                                                                                                                                                                                                                                                                                                                                            Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                             Sun,H., Abbott,A. and Le,T.P. The sequence of Homo sapiens BAC clone RP11-95D17
                                                                                  Direct Submission
Submitted (19-APR-2001) Genome Sequencing Center, Washington Submitted (19-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 190748)
                                                                                                                                                                                                             Submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                             Waterston, R.H.
Direct Submission Sequencing Center, Washington Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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76328. .165707
/note="assembly_name:Contig69"
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/chromosome="2"
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100.0%; Pred. No. 4.2e-53;
ative 0; Mismatches 0;
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                                                                                                                                    Louis,
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REFERENCE
AUTHORS
TITLE
                                                                                                                                    COMMENT
                                                                                                                                                                            JOURNAL
                                                                                                                Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Apr 19, 2001 this sequence version replaced gi:11128441.
                                                                                                                                                                                                                                   6 (bases 1 to 190748)
                                                                                                                                                                                                                     Waterston, R
                   Contact: sapiens@watson.wustl.edu
                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
Center project name: H_NH0095D17
                                                         Web site: http://genome.wustl.edu/gsc
```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap clone sections. between neighboring data submissions. This sequence was finished as follows unless otherwise noted:

οy

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence as compressions and repeats; all regions were covered by sequence than one subclone; and the assembly was confirmed by Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis McO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc restriction digest

The RPCI-II human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., at a described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., at a described a described at a finite described and improved paperoach for construction of bacterial artificial chromosome approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute The clone sequenced to the left is RP11-521D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17. (http://bacpac.med.buffalo.edu)

There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish RP11-95D17

Unresolved tandem repeat from base position 181200 to 187300. Size information from restriction digest suggests that the full repeat may not be represented.

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FEATURES
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806. .1114
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13630. .14128
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13614. ,14110
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                           EST BF770793 (NID:g12118693)"
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                                                                                  EST BF770134 (NID:g12118034)"
                                                                                                                                        EST BF770132 (NID:g12118032)"
                                                                                                              EST BF770135 (NID:g12118035)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                         Direct Submission Submitted (25 JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atch 95.1%; Score 194; DB 9; 321 Similarity 100.0%; Pred. No. 4.2e-53; 194; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                           Determination of human RANKL isoforms
                                                                                                                                                                                                                                              Ikeda, T.
                                                                                                                                                                                                                                                                                            Ikeda, T., Kuroyama, H. and Hirokawa, K.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens hranki 3 mrna for receptor activator of nuclear factor AB064268
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                                                                                                                                                                                                                                                         (bases 1 to 818)
/product="receptor activator of nuclear factor kappa
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                                       /gene="hRANKL 3"
                                                                   /gene="hRANKL 3"
                                                                                                                                      Location/Qualifiers
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Best Local Similarity
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Homo sapiens mRNA for hRANKL 2,
AB061227
                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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EVSNPSLLDPDQDATYFGAFKVRDID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Kuroyama, H.
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SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTESNGKLI
VNQDGFYYLYANICFRHHETSGDLATFYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWS
                                                                                                              GNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
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                                                                                                                                                                                                                                                                     /product="hRANKL 2"
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al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagal,M., Kyakumoto,S. and Sato,N.
Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast encoding a secreted form of ODF/TRANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchimaru, Morioka, Iwate 020-8505, Japan (E-mail:mnagal@iwate-med.ac.jp, Tel:+81-19-651.5111(ex.4436), Fax:+81-19-654-4147)
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EVSNPSLLDPDGDATYFGAFKVRDID"
184 c 200 g 260 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                        RIKQAFQGAVQKELQHIYGSQHIRAEKAMYDGSWLDLAKRSKLEAQPFAHLTINATDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="SCC-4"
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                                                                                                                                                                                                                                                                           TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
         1 (bases 1 to 954)
Dougall,W.C. and Gallbert,L.
Receptor activator of NF-.kappa.B
Patent: US 6271349-A 12 07-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                            137;
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                                                                   Unclassified.
                                                                                 Unknown
                                                                                                                               Sequence 12 from patent US AR164148
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                                                                                             Unknown.
                                                                                                                  AR164148.1 GI:16235114
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Isolated DNA molecules encoding RANK-L
Patent: US 6242213-A 12 05-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
1 (bases 1 to 954)
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AR156434
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239 c 227 g
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Query Match
Best Local Similarity
                                                                                                                                                                                                              Matches 137; Conservative
117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
                                       591 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 650
                                                                                                                    531 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTC 590
                                                            63 CAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAA 116
                                                                                                                                                          3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 47.3%;
Local Similarity 74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson,D.M. and Hughes,A.E.
Receptor activator of nf-kappa b
Patent: WO 0136637-A 12 25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 954)
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NICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGGTKYWSGNSEFHFYSIN
NICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGTTKYWSGNSEFHFYSIN
                                                                                                                                                                                                                                                                                                              VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID
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239 c 227 g
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74.58;
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RESULT 11
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                KEYWORDS
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sequence 5 from Patent W00224896.
AX451895
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                                                              AB064270 972 bp mRNA linear PRI 26-DEC-
Homo sapiens hrankL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
Homo sapiens cDNA to mRNA
                                    AB064270.1 GI:18143620
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of human RANKL isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ikeda,T. and Kuroyama,H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikeda, T., Kuroyama, H. and Hirokawa, K.
                                                                                                                                                                                                  Homo sapiens hranki 1 mrna for receptor activator of nuclear factor kappa B ligand 1, complete cds.
AB064269
Unpublished
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                AB064269.1 GI:18143618
                                      Ikeda, T., Kuroyama, H. and Hirokawa, K.
                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                   Determination of human RANKL isoforms
                                                                                                                                       Homo sapiens cDNA to mRNA.
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a 219 c 249 g 234 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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AF019047
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                                                                                                                                                                                                                                                                                                                                                                                                                                       791 ACTA 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 TGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTC 670
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                                         9367155
                                                             growth and dendritic-cell function Nature 390 (6656), 175-179 (1997) 98032977
                                                                                      A homologue of the TNF receptor and its ligand enhance T-cell
                                                                                                                       Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C., Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBose,R.F., Cosman,D. and
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                            Homo sapiens.
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Homo saplens receptor activator of nuclear
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Submisted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Immunology, Graduate
School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176,
Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                     (bases 1 to 2201)
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                                                                                                                                                                                                                                                                                                      mRNA, complete cds.
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RRSmFVALLGLGLGQVVCSVALFFYFRAQMDPWRISEDGTHCIYRILRLHENADFQDT
TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYA
NICFRHHETSGDLATEVLQLMVYVTKTSIKIPSSHTLMKGGSTKYMSGNSEFHFYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
257 c 265 g 237 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB79694.1"
/db_xref="GI:18143619"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 96.4; DB 9; Length 1034; 74.5%; Pred. No. 8.7e-21;
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                                                                                     function
                                                                                                                                                                                                                                                                                                                 factor kappa B ligand
                                                                                                                                                                                                                                                                                                                                     linear
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AF053712
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117 TGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 778
                                                                Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R., Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S., Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A., Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J., Delaney,J., and Boyle,W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation Cell 93 (2), 165-176 (1998)
                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens osteoprotegerin ligand mRNA, complete cds
                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E., Cosman,D., DuBose,R. and Galibert,L.
                                                                                                                                                                                               (bases 1 to 2271)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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429 c 497 g 617 t
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EAQPEAHLTINATDIPSGSHKYSLSSMYHDRGWAKISNMTFSNCKLIVNQDGFYYLYA
NICEFRHETSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
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srsmfvallglglgqvvcsvalffyfraqmdpnrisedgthciyrilrlhenadrodt
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129. .1082
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/db_xref="GI:2612922"
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74.5%;
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Pred. No. 8.8e-21;
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Search completed: December Job time: 553.856 secs
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     895 ACTA 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 CAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTA 834
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Boyle, W.J.

Direct Submission

Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,

Submitted (16-MAR-1998) Thousand Oaks, California 91320, USA

One Amgen Center Drive, Thousand Oaks, California 91320, USA

Location/Qualifiers
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VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"

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Perfect score:
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Listing first 45 summaries
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em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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37	38.6	84.8	95.8	Score
14.2	14.8	32.5	95.8 36.7 659	Query Match Length DB
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ALIGNMENTS

RESULT 1 AG107545 REFERENCE SOURCE VERSION DEFINITION COMMENT REFERENCE KEYWORDS ACCESSION LOCUS ORGANISM TITLE AUTHORS TITLE AUTHORS JOURNAL JOURNAL 2 (bases 1 to 659)
3 (bases 1 to 659)
4 (bases 1 to 659)
5 (colored Submission Direct Submission Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); apan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.81-45-503-9111, Fax:81-45-503-9170)
6 (Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors. Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence. AG107545 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-112G09.F. AG107545.1 GI:16728063 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y. Pan troglodytes Unpublished BAC end sequences of Library PTB 659 linear GSS 03-NOV-2001

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REFERENCE
AUTHORS
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                                                                               Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                  (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 186 row: C column: 1
                                                                                                                                                                                                                                  Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143;
Seq primer: T7
                                                                                                                                                                                                                                                                                                            Rat BAC End Sequences from Library CHORT-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-186C1.TJ
                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                  Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH267783 612 bp DNA linear GSS 30-NOV-2000.
CH230-186C1.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone_lib="PTB Chimpanzee Male BAC Library"
188 c 121 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="PTB-112G09.F"
/sex="male"
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                                row: C column: 1
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71.1%;
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Pred. No. 3.1e-21;
0; Mismatches 52;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 AGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 ACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 TCTCTCTAGGTTCCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 TATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTTCAGCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTGTACGCCAACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGG 226
                                                                                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                               Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                   Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 362)
Xu, Z., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV653073 GLC Homo sapiens cDNA clone GLCDHB01 3', mRNA sequence.
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/tissue_type="corresponding non cancerous liver tissue"
                                                  /organism="Homo sapiens\
/db_xref="taxon:9606"
/clone="GLCDHB01"
                              /clone_lib="GLC"
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"
145 c 133 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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Pred. No. 1.6e-17;
O; Mismatches 52;
                                                                                                                                                     Shanghai.
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                                                                        Best Local Similarity
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                  4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATACCATCAATATCCCATGAG 63
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RST16397 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence
BG197160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 198)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., J. (Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, Lerner,L., Costanzo,D., McElligott,K., Lo,K., Offenbacher, E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher, J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3201 Carnegie Ave, Cleveland, OH 44115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 a
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                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 148.
Location/Qualifiers
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                scain@athersys.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                         /note="See" (Treation of Genome-wide Protein Expression /note="See" (Treation of Genome-wide Protein Expression', Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the needly performed type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                           /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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77.0%;
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Pred. No. 5.6e-13;
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                                                                                  Score 38.6; DB 12; Length 198; Pred. No. 0.038;
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        2 others
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                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                        4 GCAATCCTGACGCTTCAACCTCAACTCATGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                               7 G 7
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2/6 DP MIKNE THUGE RST22738 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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BG203357.1 GI:13725044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: scain@athersys.com
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                        BG184205.1 GI:13705892
EST.
                                                                                             BG184205 2// DP MIXING SAPIERS CDNA, MRNA sequence.
BG184205
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/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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75.4%;
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pred. No. 0.15;
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Local Similarity 75.48;
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8
                     Atherays, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                             Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 29)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,
                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RST25946 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence
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                                                                                                                                                                                                     Lerner, L., Costanzo, D., McDiligott, K., Boozer, S., Whittington, J., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Goffenbacher, J., Danzig, J. and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher Creation of genome-wide protein expression libraries using random Nat. Biotechnol. 19 (5), 440-445 (2001)
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Tel: 216 431 9900
Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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scain@athersys.com
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/db_xref="taxon:9606"
/Clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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Pred. No. 0.15;
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                                                                                                                                                                                             library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end plate: 210 row: N column: 16 seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Other_GSSs: RPCI-24-210N16.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins. Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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Location/Qualifiers
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/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                                                          /sex="Male"
                                                                          /clone_lib="RPCI-24"
                                                                                          /db_xref="taxon:10090"
/clone="RPCI-24-210N16"
                                                                                                                                   /strain="C57BL/6J"
                                                                                                                                                 /organism≃"Mus musculus"
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/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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75.4%;
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Pred No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617 AGCCTCTGGGAAGGCTCTGTACTCTCCCCCGAGTGAAACACTCTGGGCGAA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGA 62
108 GGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTA 167
                                                                                                                                            698 ATAAGGATTACAAGATGAAGATAAATGGAAAGTATCCAAAACCTAAACTCACTAAGATTA 639
                                  168 CCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCT 221
                                                                                                                                                                             48 ATCAATATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTG 107
                                                                                                                                                                                                                                      Local Similarity
                                                                       GGAAATCTTCTAATACATAATAATGAGAAGAATCCATCTACTAGGAAAAGGAAAGGGTTT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOMKY36TR BO_2_3_KB Brassica oleracea genomic clone BOMKY36, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BH671765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH671765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica oleracea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
DNA is from a doubled haploid provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 724)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                               /clone_lib="BO_2_3_KB"
/clone_Tyector: pHOS1: Site_1: BstXI; 2-3 kb sheared fonce="vector: pHOS1 in pHOS1 using BstXI linkers" genomic DNA inserted into pHOS1 using BstXI linkers" 144 c 162 g 192 t
                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3712"
/clone="BOMKY36"
                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 0.5
                                                                                                                                                                                                                                          Score 34.8; DI
Pred. No. 1.3;
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                                                                                                                                                                                                                                                                 DB 17;
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                                                                                                                                                                                                                               87; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                               Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 19-FEB-2002
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SOURCE
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                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                 Query Match 13.1%; Score 34.2; DB 12; Best Local Similarity 54.3%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                         101 ATAACCAGGAATGCGAAAAGCCTTGCAGCAGCTACAAGAAGAATTGCAGAATAAGAGCCA 160
  161 ACAGCTT 167
                                               155 AAGGCAT 161
                                                                                                                                   95 ATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA 154
                                                                                                                                                                                    41 TGCAATTTGTAGAGGCTGCAGCACACGAGAGTGAACAGCAGAAAGAGGCCTTCTTGGAAAC 100
                                                                                                                                                                                                                               MR2-NT0135-131200-014-g01 NT0135 Homo sapiens cDNA, mRNA sequence. BF930674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 463)
Dias Netc,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2.NT0135-131200-014-g01&t3=2000-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                       156
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                tissue mRNA and cDNA amplification were performed under low stringency conditions."

97 c 115 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 Ludwig Institute for Cancer Research) Profiles into the puC 18 vector. Reverse transcription of profiles into the puC 18 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone_lib="NT0135"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Adult"
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RESULT 11 BM892233/c

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
141 AAAACTAAGAGTCAAAGGCATTTATTACCGG 171
                                  81 TTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGG 140
                                                                                                                                                                        21 CCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAGGCTCATAAAAACGAGTCT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                            CCTAGTTCTTAGCTCCTCAATAAGTTCATCAAGAACGCAAAATGCCAATGGCATGGCACT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: Resden, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further i call: (800)-533-4363 or contact: ccueresgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq.primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max
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                                                                                                                                                                                                                                                                                                                                                              123 a
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 /note-Tvector: pBluescript II SK+; Site_1: EcoRI; Site_2: NhOI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 9-10 day old etiolated seedlings for the cultivar Williams. Complementary DNA was poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were transformed into the EcoRI-XhoI restriction site were transformed into DH10B host cells (GibcoBRL). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 536)
                                                                                                                                                                                                                                                                                                                                                                                    Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                    library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Degenerating cotyledons, 9-10 day old eticlated seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="SOYBEAN CLONE ID: Gm-c1069-3805"/clone_lib="Gm-c1069"
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                                                                                                                                                                                                                                                                                                                                                              110 c
                                                                                                                                                                                                                                                          13.1%; Score 34.2; E 51.7%; Pred. No. 1.8;
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BE346444 475 bp mRNA linear EST 04-DEC-2001 sp25f04.yl Gm-c1042 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Agriculture and Agri-Food Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris, N., Chapman, B.P. and Gijzen, M. Gene expression in developing soybean seed coats Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: gijzenm@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1391 Sandford Street, London, Ontario, Canada N5V 4T3 Tel: 519 457 1470 Fax: 519 457 3997
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Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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//lab_host="E_coli host strain XLOLR"
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strain XLOLR.
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51.7%;
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                                               141 AAAACTAAGA 150
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                                                                                                                                                                                                                                          21 CCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAGGCTCATAAAACGAGTCT 80
  36
                                                                                              Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurt, R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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AGAACACAGA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                              1 Similarity
70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 475)
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                             from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Raiden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments sollowere transformed into DH10B host cells (Gibco BRI). This library was constructed by Dr. Randy . Shoemaker."
                                                                                                                                                                                                                                                                                              Conservative
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/clone_lib="Gm-c1042"
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Zambrowicz, B.P., Fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: exon-trapped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: materials@lexgen.com
OmniBank Sequence Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4000 Research Forest Drive, The Woodlands, TX 77381, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OmniBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Person, C. and Sands, A.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexicon Genetics Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 13.0%;
Similarity 64.8%;
                                                                                                                                                                                                                                                                                                                             AG132233
AG132233.1 GI:16661911
                                                                                                                                                                                                                                                                                                                                                                AG132233 631 bp DNA linear GSS 04-NOV-200 Pan troglodytes DNA, clone: PTB-144117.F, genomic survey sequence.
submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (SSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                    Totoki,Y., Watanabe,H. and Sakaki,Y Direct Submission
                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                     Pan troglodytes
                                                                                     Fujiyama, A.,
                                                                                                                          Unpublished
                                                                                                                                              BAC end sequences of Library PTB
                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
                                                                                                             (bases
                                                                                                                                                                                                                                                                      troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-144117.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST1450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="embryonic stem cell" 118 c 119 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                         1 to 631)
                                                                                                                                                                                                                                     Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                         Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedrich, G.A., Buxton, E.C., Lilleberg, S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 bp
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Search completed: December 8, 2002, 19:27:07 Job time: 589.736 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                             Query Match 13.0%; Score 34; DB 17; Length 631; Best Local Similarity 57.5%; Pred. No. 2.3; Matches 61; Conservative 0; Mismatches 45; Indels
                                                                 173 TCAAACTTCGTTGATAGAAGGAAATGTAAGTTTAGGGAGAGTGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                   99 CCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY
                                                                                                                                                                                                                                                                                                                    181 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing: -21M13
                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/clone_lib="9TB Chimpanzee Male BAC Library"
/clone_lib="98 g 202 t 2 others
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/db_xref="taxon:9598"
/clone="PTB-144I17.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .631
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Minimum DB seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
N_Geneseq_101002:*

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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

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Gapop 10.0 , Gapext 1.0
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261
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9 121.2	8 121.2	7 121.2	6 121.2	5 121.2	4 121.2	3 121.2	2 121.2	1 251	Result No. Score	
46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	96.2	Query Match Length DB	æ
1945	954	954	954	954	954	954	741	1186	Length	
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ABK12877	AAD05904	AAD08715	AAD15311	AAV41372	AAV41378	AAV69887	AAV69899	ABK33576	ID	
cDNA encoding huma	Human full-length	Human receptor act	Human receptor act	NF-kB receptor act	NF-kB receptor act	Nucleic acid encod	Nucleic acid encod	cDNA encoding huma	Description	

Human prostate exp	ABV23301	23	351			c 45	
CER encoding CDNA.	AAX18560	20	3405	13.9	36.2	44	
sequence	വ	20	2291	13.9	•	43	
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encoding o	AAZ99973	21	519	24.1	σ	41	
encoding	AAZ99970	21	564	28.2	w	40	
encoding	AAZ99967	21	564	28.2	ω -	39	
0	AAZ99971	21	546	28.2	73.6	38	
	AAZ99972	21	519	28.2	ω ·	37	
encoding	AAZ99969	21	519	28.2	ω	36	
a	AAZ99968	21	519	28.2	ω.	<u>ა</u>	
Mouse OBM nucleoti	AAA39155	21	2029	31.3	۲.	34	
Mouse cDNA encodin	AAS13369	22	522	34.9	9	ω ω	
DNA encoding a mur	AAZ99966	21	2299	36.6	Û	32	
Human osteoprotege	AAV70284	19	2295	36.6	G	31	
cDNA encoding mous	ABK12880	24	2237	36.6	5	30	
Murine TRANCE enco	AAX80224	20	2237	36.6	5	29	
	AAV41489	19	2191	36.6	95.6	28	
Murine RANKL (rece	AAD05903	22	1630	36.6	5	27	
	AAD08714	22	1630	36.6	Ŋ	26	
	AAD15310	22	1630	36.6	ū	25	
н	AAV41371	19	1630	36.6	رن د	24	
receptor	AAV41377	19	1630	36.6	ū	23	
	AAH25526	22	1574	36.6	UT.	22	
Nucleic acid encod	AAV69886	19	1538	36.6	ري.	21	
Osteoclast formati	AAZ49024	21	951	36.6	5	20	
DNA encoding a mur	AAZ99965	21	951	36.6	5	19	
Mouse OBM nucleoti	AAA39156	21	951	36.6		18	
Nucleotide sequenc	AAV69900	19	951	36.6		17	
Nucleic acid encod	AAV69898	19	735	36.6		16	
Rat osteoclast dif	AAF86481	22	957	39.1		15	
Human TRANCE encod	AAX80223	20	1823	45.2	_	14	
cDNA encoding huma	ABK40274	24	2390	46.4	_	13	
Human osteoprotege	AAV70285	19	2274	46.4		12	
DNA encoding a hum	AAZ99964	21	2271	46.4	121.2	11	
cDNA encoding huma	ABK12876	24	2226	46.4	121.2	10	

ALIGNMENTS

PR PR PR PR	אַ אָקי אָקי	XX PF XX XX	PN	KW KW	DEXX	DT X AC X	RESU ABK3 ID
25-JUL-2000; 2000US-220634P. 25-JUL-2000; 2000US-220638P. 25-JUL-2000; 2000US-220664P. 25-JUL-2000; 2000US-220666P. 26-JUL-2000; 2000US-220893P.			Homo sapiens. WO200208288-A2.	Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.	cDNA encoding human PRO protein, Seq ID No 81.	ABK33576; 08-MAY-2002 (first entry)	RESULT 1 ABK33576 standard; cDNA; 1186 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour prostate tumour, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC the proliferation of, or gene expression, in pericyte cells, for stimulating the relases of tumour necrosis factor-alpha from human blood, CC for stimulating or inhibiting the proliferation of normal human dearmal CC fibroblast cells. The PRO polypeptide may also be used as molecular CC applications in molecular biology, including use as hybridisation probes, CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human CC PRO protein coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;
                                                                                                                                                                                                                                                         447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000;
23-AUG-2000;
24-AUG-2000;
15-SEP-2000;
10-NOV-2000;
 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Figure 81; 359pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour or liver tumour -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grimaldi JC,
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01-DEC-2000;
                                                                                                                                                                                                                 61 GAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCC 120
                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                 1 ATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATACCATCAATAATCCCAT 60
                                                                                  ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGG 240
                                                                                                                                                                                  TGTAATTTGAG 251
                                                                                                                                     AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTATCCGGAATGCCGAC 180
TGTAATTTGAG 697
                                                       ATGCCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCAT 506
                                                                                                                      AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-172001/22.
DB; AAU83632.
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C, Gurney AL,
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2000WO-US23522
2000WO-US23328
2000US-000000P
2000WO-US30873
2000WS-US30873
2000WS-US32678
2000WS-US32678
2000WS-US32678
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2001US-0854280
                                                                                                                                                                                                                                                                                                                                     96.2%; Score 251; 100.0%; Pred. No.
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT

Qy 밁 QΥ

64 GCT--CATAAAACGAGTCTTTCTTCGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121

4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG

Matches Query Match Best Local

181;

Conservative

0;

Mismatches

53;

Indels

œ ..

Gaps

2

319

Similarity

46.48; 74.88;

Score 121.2; DB 19; Length 741; Pred. No. 1.4e-30;

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AAV69899
                                    The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone of the protein, for investigative and diagnostic purposes, and as
Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;
                                   components of drugs.
                                                                                                                                                                                                                                                           Example 28; Pages 121-122; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                              Nakagawa N, Shima N, Takahashi K
Washida N, Yamaguchi K, Yano K,
                                                                                                                                                                                                                                                                                                      Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L5-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Higashio K,
N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone absorption factor; bone disorder; calcium metabolism;
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97JP-0097808.
97JP-0151434.
97JP-0217897.
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1..741
                                                                                                                                                                                                                                                                                                                                                                                         N, Takahashi K, Tomoya
vano K, Yasuda H
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Tsuda E;
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                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1997;
09-JUN-1997;
12-AUG-1997;
                                                                 The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins absorption factor by separation and solubilisation of membrane proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule;
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                                                                                                                                                                                                                Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                Goto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1997;
                                                                                                                                                                      Claim 38; Page 115; 151pp; Japanese
                                                                                                                                                                                                                                                           P-PSDB; AAW83018.
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           affinity chromatography using OCIF. It exists in a full-sequence and a solubilised form (sOBM) which is a shorter chain. OBM may be for screening potential inhibitors and modifiers of its biological vity, and screening for receptors to OBM which mediate its function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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K, Yano K, Y
be used
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asuda H;
the treatment of disorders
                                                                                                                                                                                                                                                                                                                                Morinaga
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RESULT 4
AAV41378
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                                                                                                                                               14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function and calcium metabolism. The antibodies can be used of the protein, for investigation and discrete.
         New isolated ligand for receptor activator of NF-kappa develop products for augmenting an immune response for inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                           RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
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                                                                                                Anderson DM,
                                                                                                                                                                                                 22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV41378 standard; cDNA; 954
                                                             P-PSDB;
                                                                       WPI; 1998-377657/32.
                                                                                                                      (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                Galibert
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96US-0059978.
97US-0813509.
                                                                                                                                                                                                 97WO-US23775
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                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                         /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                       /*tag=
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74.88;
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                                                                                                Maraskovsky
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                      inhibiting
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RESULT 5
AAV41372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                               WO9828424-A2
                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                 RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GCT--CATAAAACGAGTCTTTCTTCGAAAACATGACCAAGATTGGGCAAACGTCTCCA 121
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Local Similarity 74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG
                                                                                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                      response; in RANK ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                          /product= "human RANKL (ligand for RANK)"
                                                                                                                                         /*tag=
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to
                                                                                                           AAD15311 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW68293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory response, treating toxic shock or sepsis
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                                                                                                                                                                                                      713 TA 714
                                                                                                                                                                                                                                       236
                                                                                                                                                                                                                                                                         653 CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
                                                                                                                                                                                                                                                                                              176 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GCT--CATAAAACGAGTCTTTCTTCGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 46.4%;
Local Similarity 74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACATCATCAATATCCCATGAG
                                                                                                                                                                                                                                       TA 237
                                                                                                                                                                                                                                                                                                                                                                     ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                  ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0064671.
96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maraskovsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121.2; DB 1
Pred. No. 1.5e-30;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19; Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
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Human receptor activator of NF kappaB ligand (RANKL) cDNA

15-NOV-2001 (first entry)

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The patent discloses novel receptor activator of nuclear factor (NF)-CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member CC of the tumour necrosis factor (TNF) receptor superfamily and associates (CC with TNF receptor associated factor (TRAF) 2 and 3 which are important CC in the regulation of immune and inflammatory response. The receptors CC are useful for regulating immune response and in screening for inhibitors of signal transduction, e.g. for screening the CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists CC are useful in ameliorating the negative effects of an inflammatory CC response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory CC reactions and the effects of bone resorption. RANK from apoptosis. CC soluble forms of the receptor are used in vivo or in vitro based CC screening tests for agonists or antagonists of RANK acts as an anti-CC adjunct therapy for disease characterised by neoplastic cells that CC express RANK. Compounds that interfere with RANK/TRAF6 interactions are used in the CC are used as inhibitors of disease characterised by neoplastic cells that CC express RANK. Compounds that interfere with RANK/TRAF6 interactions CC are used as inhibitors of disease sassociated with excess bone resorption and activites. They are useful for the expressants or anti-inflammatory agents. The RANK DNAs are used in preparing kits for the detection of soluble RANK, or another RANK. Parak compositions as probes for analysis of the presence or distribution of RANK transcripts, while the proteins CC monitor RANK-related activity. The present sequence is a cDNA encoding thus to the detection of soluble RANK, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct the approximately adjunct the approximately approximately the cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1996;
07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Column 69-71; 47pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1996;
07-MAR-1997;
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human RANK ligand (RANKL)
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97US-0813509.
97US-0996139.
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97US-0064671
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/product= "Human RANK ligand (RANKL) protein"
protein
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RESULT 7
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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 954 BP; 255 A; 239
                                  Claim 2; Column 61-64; 43pp; English.
                                                          New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human receptor activator of NF-chi B ligand (huRANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD08715 standard; cDNA;
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                                                                                                                                                                          (IMMV ) IMMUNEX CORP.
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                                                                                                            2001-407216/43
DB; AAE04426.
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97US-0077181.
97US-0064671.
                                                                                                                                                                                                                                                   97us-0995659
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/product=
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74.88;
                                                                                                                                                                                                                                                                                                                             "Human RANKL protein"
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Pred. No. 1.
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nes 53; Indels
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The present invention relates to receptor activator of NF-chi B (RADNA, RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to

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RESULT 8
AADO5904
ID AADO
XX AADO
XX AADO
XX AADO
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XX Hunna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huranKL)
Anderson DM,
                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                             17-NOV-1999;
                                                                                                                                                                                                           14-NOV-2000; 2000WO-US31459.
                                                                                                                                                                                                                                                                                                                                             WO200136637-A1
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      Hughes AE
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of NF-kappaB ligand) protein"
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Pred. No. 1.
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es 53; Indels
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RESULT 9
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           Human; tumour necrosis factor-related activation induced cytokine; TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset paget's disease of bone (EP). The present sequence is a cDNA encoding full-length human RANKL (hurankl) protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor-associated factors (TRAFS). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system.
                                                                                                                                             cDNA encoding human TRANCE protein splice variant 2.
                                                                                                                                                                                           18-JUN-2002
                                                                                                                                                                                                                                        ABK12877;
                                                                                                                                                                                                                                                                                ABK12877 standard; cDNA; 1945
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                                                                                                                                                                                                                                                                                                                                                                                                                                     236
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Local Similarity 74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTAATAACACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                     TA 237
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Pred. No. 1.5e-30;
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                                                                                                                                                                                                                                                                                           (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and one or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 2, of the invention. TRANCE is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200216551-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001; 2001WO-US26101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the mammal a tumour necrosis factor-related activation induced cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAU78286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other;
                                                                                                                                                                                                                                                                                    family and acts
                                   408
122 ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG
                                                                    64
                                                                                                                                                                                                                                                                        of the invention. TRANCE is a member or the nily and acts directly on cartilage-producing
                                                                                                                                          4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-304119/34.
                                   GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCA
                                                                    GCT--CATAAAACGAGTCTTTCTTCGTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                       GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 407
                                                                                                                                                                              181;
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                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odgren PR,
                                                                                                                                                                              Conservative
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/*tag= b

/note= "Target region for antisense

95..829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Tumour necrosis factor (ligand) superfamily,
    member 11 (TNFSF11), Specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*taq=
                                                                                                                                                                                           46.48;
74.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marks SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human TRANCE (tumour necrosis factor-related activation induced cytokine) protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splice variant 2"
                                                                                                                                                                            0
                                                                                                                                                                                                             Score 121.2;
                                                                                                                                                                                            Pred. No.
                                                                                                                                                                          Mismatches
                                                                                                                                                                                            2e-30;
                                                                                                                                                                                                             DB 24;
                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                cells (chondrocytes).
                                                                                                                                                                            Indels
                                                                                                                                                                                                             Length 1945;
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                                                                                                                                                                            8;
                                                                                                                                                                          Gaps
                                   467
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RESULT 10
ABK12876
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     the mammal a tumour necrosis factor-related activation induced cytokin (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive carrilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy; bone damage; cartilage damage; traumatic injury; surgery; osteoarthrit rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to
                                                                                                                                                                                              cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding human TRANCE protein splice variant 1.
                                                                                                                                                                                                                                                                                                           Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cartilage growth; skeletal growth; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; tumour necrosis factor-related activation induced cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK12876 standard; cDNA; 2226 BP
                                                                                                                                               Disclosure; Fig 1; 55pp; English.
                                                                                                                                                                             cytokine-modulating agent to mammal -
                                                                                                                                                                                                                           Treating mammal having disorder characterised by abnormal
                                                                                                                                                                                                                                                                             WPI; 2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                         18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001; 2001WO-US26101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200216551-A2
                                                                                                                                                                                                                                                                                                                                           (UYMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC
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                                                                                                                                                                                                                                                                                                                                           UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                                                                                                                                                                                                           Odgren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 141..190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                              Marks SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activation induced cytokine) protein splice variant 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for antisense
                                                                  cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587
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Best Local
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WPI; 2000-271444/23
                              Halkier T,
                                                                                           15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                        Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 craniofacial-skeletal discrepancies and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and discorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor feature and acted affector.
                                                                                                                                                                                                        WO200015807-A1.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a human osteoprotegerin ligand (OPGL).
                                                            (MEBI-) M & E
                                                                                                                                                                                                                                                                                                                                            immune response; osteoporosis; bone resorption; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ99964 standard; DNA; 2271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2226 BP; 656 A; 448 C; 505 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΤA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCAAGATCTCCA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                             Haaning J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                            BIOTECH AS
                                                                                           98DK-0001164.
98US-0102896.
                                                                                                                                       99WO-DK00481
                                                                                                                                                                                                                                  /product= "osteoprotegerin ligand"
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%;
74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24; Length 2226;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce the content of the con
                       W09846751-A1
                                                                                                                                                                                                                                                                                             Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                              Paget's
                                                                                                                                                                                                                                                                                                                                                                                                                Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV70285 standard; DNA; 2274 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2271 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 TA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               657 GCAAGCTTGAAGCTCTAGCTCATCTCACTATTAATGCCACCGACATCCCATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treat, prevent and ameliorate osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGGTTGGGCCCAAGATCTCCA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898
                                                                                                                                                                                                                                                                              disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                 Location/Qualifiers 185..1138
                                                                         /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            658 A; 462 C; 522 G; 629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.48;
74.88;
                                                                      "osteoprotegerin binding
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Pred. No. 2.1
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                                                                      protein"
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ABK40274
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AC ABK4
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Best Local S
Matches 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding osteoprotegrin binding protein – useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1998;
16-APR-1997;
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P-PSDB; AAW83195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses,
 ABK40274;
                                  ABK40274 standard; cDNA; 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
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                                                                                                                                                                                                                                                                                                                                                                                                       GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 716
                                                                                                                                                                                                               CCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGC
                                                                                                                                                                                                                                                                                                  ACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTTATTACCGGAATG 175
                                                                                                                                                                                             CCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAAC
                                                                                                                                                                                                                                                                 ACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG
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97US-0842842.
97US-0880855.
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74.88;
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Pred. No. 2.1
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Best Local
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22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
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15-SEP-1999;
30-NOV-1999;
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11-MAR-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                             polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc.), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                           Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002 (first entry)
                                                                                                         Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                    Claim 50; Fig 41; 302pp; English.
                                                                                                                                                                                                                                                                                                              malignancies, inflammatory, angiogenic and immunologic
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                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                          Marsters
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                                                                                                                                    polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
 778
                           4 GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCATGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding human PRO206 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                  2002-205567/26.
GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTG 837
                                                       181;
                                                                   Similarity
                                                      Conservative
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99US-149395P
99US-151689P
99WO-US20111
99WO-US21090
99WO-US28313
99WO-US28301
                                                                                                                                                                                                                                                                                                                                                                                                                          Pan J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-145698P
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99US-140653P.
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                                                                46.48;
74.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski PJ,
i RM, Roy MA,
                                                      0; Mismatches
                                                                Score 121.2;
Pred. No. 2.2
                                                                 2.2e-30
                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney AL,
Smith V,
                                                                                 DB 24;
                                                    53;
                                                       Indels
                                                                               Length 2390;
                                                                                                                                                                                                                                                                                                                                                                                                                            Stone DM;
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64 GCT--CATAAAACGAGTCTTTCTTCGTAGAAACATGACCAAGATTGGGCAAACGTCTCCA 121

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RESULT 14
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                                        The present sequence encodes human TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially confirmance).
                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
Sequence 1823 BP; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                                                                                                                                                                                                                                            Claim 1; Fig 1; 164pp; English.
                                                                                                                                                                                                                                                                                                                                           Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1998;
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                                                                                                                                                                                                                                                                   TNF like proteins for treating autoimmunity and cancer
                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
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                                   or TNF-alpha).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding cDNA.
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97US-0989479.
98US-0034099.
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       305 C;
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380 G; 569 T; 0 other;

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Best Local Similarity
The present sequence is the coding sequence for rat Osteoclast Differentiation Factor (ODF). ODF is thought to be directly involved in the differentiation of monocytes/narcophages into osteoclasts. Osteoclasts promote dissolution of the bone matrix and solubilisation of bone salts. The present sequence is useful in gene therapy, and as hybridisation probes or primers. ODF protein is useful for modulating the
                                                                                                   Claim 1; Fig.1; 81pp; English.
                                                                                                                                      Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation,
                                                                                                                             cell differentiation and cell viability
                                                                                                                                                                                     P-PSDB; AAB82092
                                                                                                                                                                                                                             Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; osteoclast formation inducer;
Osteoclast Differentiation Factor;
                                                                                                                                                                                                                                                        (UYWA-) UNIV WESTERN AUSTRALIA.
                                                                                                                                                                                                                                                                                   29-SEP-1999;
                                                                                                                                                                                                                                                                                                             29-SEP-2000; 2000WO-AU01202
                                                                                                                                                                                                                                                                                                                                        05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat osteoclast differentiation factor, ODF, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF86481;
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                                                                                                                                                                                                                             Zheng M;
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Pred. No. 2.3e-29;
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                                                                                                                                                                                                                                                                                                                         activity of cells, e.g., cell proliferation, cell differentiation and cell viability, as immunogens to generate anti-rat ODF antibodies, and as vaccines. Anti-rat ODF antibodies are useful in assay methods for quantifying ODF polypeptides.
                                                                                                                                                                                                                                                                                               Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;
                                                                                           715 CT 716
                       235
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                                                          175 GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG 234
                                            GCCAACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACTATCTTCAG 714
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Search completed: December 8, 2002, 17:26:15 Job time: 81.3192 secs

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Title:
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Gapop 10.0 , Gapext 1.0
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261
1 atggcaatcctgacgctcag.....gtaatttgagaatcattcac
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score 249.4 121.2 121.2 121.2 121.2 121.2 121.2 121.2 121.2 121.2 121.2 121.2 121.2 121.2 84.8 81.6 81.6 81.6 37.2 Match Length Query 113451 200724 951 951 951 1630 1630 1630 2191 2191 2225 2225 2299 165707 190748 2029 2029 276831 142588 113451 166759 169960 127812 972 1034 2201 2271 2390 DΒ 0000000 10 ω ω ω ω 10 2 9 9 10 10 10 10 10 10 AL139382) AB032772) AB032771 AX358828 AX362321 AC104794 AX140162 AF019048 AF013170 AB064270 AB064269 AR164148 AX147989 AB061227 AB037599 AR062119 AF053713 AF187319 AC023297 AC094149 E34349 AF013171 AX451897 AR157058 E36388 AX451895 AR156434 E34350 AX201362 AF053712 AB064268 AR156433 AX147987 AR164147 SUMMARIES ALIGNMENTS AB032772 Mus muscu AB032771 Mus muscu E34350 DNA and pro E36388 Novel prote AX451897 Sequence AX157058 Sequence AX157058 Sequence AX160162 Sequence AF019048 Mus muscu AF013170 Mus muscu AR062119 Sequence AF053713 Mus muscu AB061227 AB037599 AR156434 AR164149 AR147989 AX451895 AX451895 AB064270 AB064270 AB064270 AB063712 AX201362 AX362321 AC104794 AC010969 E34349 DNA and pro AB022039 Mus muscu AC126690 Mus muscu AC113992 Mus muscu AC023397 Homo sapi AC007716 Homo sapi AC006440 Homo sapi Description AB064268 AR156433 Sequence AR164147 Sequence AX147987 Sequence AC023297 Homo sapi AL139382 Human DNA AF013171 AX232589 Sequence AC094149 Rattus no AF013171 Homo sapi AF187319 Rattus no AB008426 Mus muscu AB036798 Mus muscu Sequence Sequence Sequence Sequence Homo sapi Sequence Homo sapi Homo sapi Sequence Homo sapi Homo Homo sapi Homo sapi sapi

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REFERENCE AUTHORS	SOURCE	RESULT 1 AX358828 LOCUS DEFINITION ACCESSION VERSION
1 Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX358828 1186 bp DNA linear PAT 13-FEB-2002 Sequence 81 from Patent W00193983. AX358828 AX358828.1 GI:18675315

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                                                                                 1 ATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCAT 60
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                                                      ATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCAT 506
                                                                                                                   251; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTAATTTGAG 697
                                                                                                                                                                                                                                                                                             Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.

Secreted and transmembrane polypeptides and nucleic acids encoding
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                                                                                                                                                                                                                                                                                            the same
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                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon;9606"
                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                        Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162662 bases at least 040
Consensus quality: 163189 bases at least 030
Consensus quality: 164786 bases at least 020
Insert size: 9479; agarose-fp
Insert size: 167795; sum-of-contigs
Quality coverage: 12.78 in 020 bases; sum-of-contigs
Quality coverage: 10.53 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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Submitted (30-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Sulston, J.E. and Waterston, R.
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submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                            Waterston, R.H.
Direct Submission
                                                                                                       The sequence of Homo sapiens BAC clone RP11-95D17
                                                                                                                           Sun, H., Abbott, A.
                                                                                                                                                                                       Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                   Homo sapiens
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13 76227: contig of 75015 bp in length
8 76327: gap of unknown length
8 165707: contig of 89380 bp in length.
Location/Qualifiers
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76328. .165707
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/chromosome="2"
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Waterston,R.H.
Direct Submission
Submitted (19-APR-2001) Genome Sequencing Center, Washington
Submitted (19-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                        MO 63108,
5 (bases
                                                                                                                                   Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 on Apr 19, 2001 this sequence version replaced gi:11128441
                                                                                                                                                                                                                                                                                                                          Waterston,R.H.
Direct Submission
Submitted (20-APR-2001) Genome Sequencing Center, Washington
Submitted (20-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                       Contact: saplens@watson.wustl.edu
                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
Center project name: H_NH0095D17
                                                                  Web site: http://genome.wustl.edu/gsc
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                             Summary Statistics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-521D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17. (http://bacpac.med.buffalo.edu) рвасез.6

There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish redundant clone AC062035. Data from AC062035 was used

RP11-95D17

may not be represented Unresolved tandem repeat from base position 181200 to 187300. Six information from restriction digest suggests that the full repeat

/db_xref="taxon:9606' /organism="Homo sapiens" Location/Qualifiers .190748

/chromosome="2"

FEATURES source

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12955. .13065
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!2467. .12594
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l1424. .11704
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9322. .9647
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7701, .8007
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4196. .5255
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2626. .3646
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185. .230
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/clone="RP11-95D17"
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Db 174245 TGTAATTTGAG 174235
                                           Db 174365 AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGAC 174306
                                                                                                                                                      Matches 250; Conservative
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Best Local Similarity
                                                                                                                  121 AACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGGAATGCCGAC 180
                                                                                                                                                                                                                                                                                                                                                             misc_feature
                          241 TGTAATTTGAG 251
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13614. .14110
/note="similar to
13623. .14122
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14851. .15156
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                                                                                                                                                                                                                                                                       Score 249.4; DB 9; Length 190748;
Pred. No. 7e-68;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                      EST BF699834 (NID:g11985242)
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1

AUTHORS Ikeda, T., Kuroyama, H. and Hirokawa, K.

Determination of human RANKL isoforms

REFERENCE 2 (bases 1 to 818)

AUTHORS Ikeda, T. and Kuroyama, H.
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ACCESSION VERSION KEYWORDS SOURCE

AB064268.1 GI:18143616
Homo sapiens cDNA to mRNA.

DEFINITION

Homo sapiens hranki 3 mrNa for receptor activator of nuclear factor ABD 64258

AB064268

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Local Similarity 74.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCT--CATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA 121
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Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578
                                                              Ikeda, T. and Kuroyama, H. Direct Submission
                                                                                                                                                                                                                                                                                                                 AB061227.1 GI:16610212
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens mRNA for hRANKL
                                                                                                                        Unpublished
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                      Homo sapiens cDNA to mRNA.
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                                                                                                                                             Human RANKL isoform
                                                                                                                                                                 Ikeda, T., Kuroyama, H. and Hirokawa, K
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EVSNPSLLDPDQDATYFGAFKVRDID"
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/protein_id="BAB79693.1"
/db_xref="G1:18143617"
/db_xref="G1:18143617"
/translation="MpprarisebgTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR
RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDI
PSGSHKVSLSSWYHDRGWAKISNMTESNGKLIVNQDGFYYLYANIGFRHHETSGDLAT
PSGSHKVSLSSWYHDRGWAKISNMTESNGKLIVNQDGFYYLYANIGFRHHETSGDLAT
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84. .818
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/db_xref="taxon:9606"
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                                                                     Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchimaru, Morioka, Iwate 020-8505, Japan (E-mail:mnagai@lwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)
                                                                                                                                                  Nagai, M., Kyakumoto, S. and Sato, N. Direct Submission
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                     encoding a secreted form of ODF/TRANCE
                                                                                                                                                                                                                                                                                         Cancer cells responsible
                                                                                                                                                                                                                                                                                                         Nagai, M., Kyakumoto, S. and Sato, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB037599.1 GI:6863047
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VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWS
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/product="hrankL 2"
/protein_id="BaB71768.1"
/protein_id="BaB71768.1"
/db_xref="GI:16610213"
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/translation="MFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL
/translation="MFVALLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL
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/db_xref="taxon;9606"
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                                                  Location/Qualifiers
/db_xref="taxon:9606"
                /organism="Homo sapiens"
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GCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCCACCGACATCCCATCTG 532
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Isolated DNA molecules encoding RANK-L Patent: US 6242213-A 12 05-UUN-2001;
                                                                                                                                                                                                                                                                                                                                954 bp
Sequence 12 from patent US 6242213.
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RIKQAFGGAVQKELQHIYGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDI
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EYLQLAVYYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
EVSNPSLLDPDQDATYFGAFKVRDID"

184 c 200 g 260 t 3 others
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95. .829
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/tissue_type="tongue"
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    Eukaryota; Metazoa;
Mammalia; Eutheria;
                               Homo sapiens
                                                                                       Sequence 12 from Patent W00136637 AX147989
                                               human
                                                                        AX147989.1 GI:14346964
                                                                                                                    AX147989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor activator of NF-.kappa.B Patent: US 6271349-A 12 07-AUG-2001;
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Dougall, W.C. and Galibert, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
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239 c 227 g
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity
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Anderson, D.M. and Hughes, A.E.
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                                                                                                                                                                                                                                                                                                                                                               954 bp
Sequence 5 from Patent WO0224896.
AX451895
                                                                                                                                                                                                                                                                                                                                                    AX451895.1 GI:21698735
                                                                                                                                                                                   of nf-kb
                                                                                                                                                                                                  Screening assays for agonists or antagonists of receptor activat or
                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                               CORPORATION (US)
                                                                                                                                                                WO 0224896-A 5 28-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="cAc41185.1"
/db_xref="g1:4346965"
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EAQPFAHLTINAPDIPSGSHKVSLSSNYHDRGMAKISMYFSNGKLIVUQDGFYYLYA
NICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
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239 c 227 g 233 t
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/protein_id="CAD37794.1"
                                     /note="unnamed protein product"
                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                    /codon_start=]
                                                                                                                                                                                                                                                                          Metazoa;
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Primates;
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Pred. No. 2.8e-27;
0; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB064270 972 bp mRNA linear PRI 26-DEC Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear factor kappa B ligand 2-2, complete cds.
                                                                                                                                                                                                                                                                       Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                          Ikeda, T. and Kuroyama, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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srsmfvallglglgovvcsvalffyfraqmdpnrisedgthciyrilrlhenadfodt
tlesqdtklipdscrrikqafqgavqkelqhivgsqhiraekamvdgswldlakrskl
eaqpfahltinatdipsgshkvslsswyhdrgwakismvtfsncklivnodgfyylya
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VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
                                                                                                                                 /gene="hRANKL 2-2"
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                                                                                                               /gene="hRANKL 2-2"
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                          Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens hRANKL 1 mRNA for kappa B ligand 1, complete cds. AB064269
                                                                                                                                                                                                                                                                                                                                Fax:81-3-5803-0123)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          keda, T. and Kuroyama, H.
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EaqpfahlTinatdipsgshkvslsswyhdrgwakisnwtfsngklivnqdgfyylya
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SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISINWTESNCKLI
VNQDGFYXLYANICERHHETSGDLATEYLOLMVYVTKTSIKIPSSHTLMKGGSTKYWS
GNSEFHFYSINVGGFFKLRSGEELSIEVSNPSLLDPDQDATYFGAFKVRDID"
a 219 c 249 g 234 t
                                                                                                                                                          /gene="hRANKL 1"
/codon_start=1
                                                                                                                                     /product="receptor activator of nuclear factor
                                                                                                                                                                                                                 /gene="hRANKL 1"
                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                        ′organism="Homo sapiens"
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Pred. No. 2.8e-27;
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                                                                                                                                                                                                                                   Submitted (13-AUG-1997) Molecular Biology, University St., Seattle, WA 98101, USA
                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                             Cosman, D., DuBose, R. and
                                                                                                                                                                                                                                                                                                                                                     growth and dendritic-cell functio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens receptor activator (RANKL) mRNA, complete cds. AF019047
                                                                                                                                                                                                                                                                                           Anderson, D.M.,
                                                                                                                                                                                                                                                                                                                            9367155
                                                                                                                                                                                                                                                                                                                                                                                  A homologue of the TNF receptor and
                                                                                                                                                                                                                                                                                                                                                                                                             Tometsko, M.E., Roux, E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, D.M., Maraskovsky, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
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(bases 1 to 2201)
derson,D.M., Billingsley,W., Dougall,W.,
nnRose,R. and Galibert,L.
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VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID"
a 257 c 265 g 237 t
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                                                                                                                                                                            /organism="Homo sapiens"
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                                          /codon_start=1
                                                                      /note="receptor activator
                                                                                     /gene="RANKL"
                                                                                                    /gene="RANKL"
129. .1082
                                                                                                                                             /map="13q14"
                                                           .igand"
                                                                                                                                                                /chromosome="13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
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Pred. No. 2.
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of nuclear factor kappa
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Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,
Delaney,J. and Boyle,W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)
98227661
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SRSMFVALLGLGLGOVVCSVALFFYFRAMDPRISEDGTHCIYRILRLHANDFODT
TLESQDTKLIPDSCRRIKOAFOGAVOKELOHIVGSOHIRAEKAMVDGSWLDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLJA
NICFRHHETSGDLATEYLQLAVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLKRSGEISIEVSURSLLDPOQDATYFGAFKVRDID"

4 29 c 497 g 617 t
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
185. .1138
                   /product="osteoprotegerin ligand"
/protein_id="AAC39731.1"
/db_xref="GI:3057146"
                                                                                                       activation"
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translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA/
                                                                               /codon_start=1
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EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISMMFFSNGKLIVNQDGFYYLYA
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Perfect score:
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SUMMARIES

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44	46.4	48	75.8	84.8	95.8	Score
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9 AA337226	в92778	BF724774	AV653073	BH267783	AG107545	DB ID
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AQ021146 CIT-HSP-2 AQ021146 CIT-HSP-2 F03748 HSC28F022 n AQ580608 RPCI-11-4	Home 2978	ALZUBUS GIRECUS.A AW749542 QV4 BET040 BQ182337 UI-H-EUO- AG173653 Pan trog1 BW666955 UI-E-Cl1-	0150 0767 0697 5966	081027 QV1-BT06	Pan HS_5	RST31	qi02g09	RPCI	Tetraodo 28L3-T7 I		197160 RST163 669724 HS_538 013160 CIT-HS	9 EST3783 3 HS_2164 6 Drosoph

ALIGNMENTS

COMMENT	TITLE JOURNAL	REFERENCE AUTHORS		REFERENCE AUTHORS	ORGANISM	w	RESULT 1 AG107545 LOCUS DEFINITION ACCESSION VERSION
1-7-22 Suchiro-chou, Tsuruni-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail-chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of	Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (FIKEN). Genomic Sciences Center (GSC);	Z (bases 1 to 659) Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.	DACK end sequences of Library PTB Unpublished	1 Tujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki v. Watanaho u and Sakaki v	BAC Library clone:PTB-112609.F. Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	GSS. Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male	AG107545 659 bp DNA linear GSS 03-NOV-2001 Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence. AG107545 AG107545 1 GI:16728063

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 GGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAGGAT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 GCTACAGAATATCTTCAACTA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     702 ACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       588 GATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 ATGCCTCTCTTCTCCACAGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGG 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143;
                                                                             9712 Medical Center Dr., Rockville, MD 20850, USA
rel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                               (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 186 row: C column: 1
                                                                                                                                                                                                                                                                                                             Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999) Other GSSs: CH230-186C1.TJ
                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 612)
1 (bases 1 to 612)
2hao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH230-186C1. TV CHORI-230 Segment 1 Rattus norvegicus CH230-186C1, DNA sequence. BH267783
Seq primer: T7
                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                         ,A., Gebregeorgis,E., Overton,L.,
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
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R.Site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_lib="PTB Chimpanzee Male BAC Library"
168 c 121 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pan troglodytes"
/db_xeef="taxon:9598"
/clone="ptb-112609.F"
/sex="male"
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SacI
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Pred. No. 1.
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Sciurognathi; Muridae; Murinae;
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ches 52;
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AV653073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 ATCTTCAGCT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 ACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 AGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 TCTCTCTAGGTTCCCATAAAGTCAGTCTGTCCTCTTGGTACCATGATCGAGGCTGGGCCA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hes 132;
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                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human Genor
351 Guo Shoujing Road, Zhan,
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTGTACGCCAACATTTGCTTCAGGCATCATGAAACCTCAGGGAGCGTACCTGCGGACT 424
                                                                                                                                                                                                                                                                                                                               Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV653073 GLC Homo sapiens cDNA clone
                                                                                                                                                                          Email: hanzg@chgc.sh.cn
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                                                                                                                                 clone is available at CHGC in
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCDHB01"
                                                                                                                 1. .362
/tissue_type="corresponding non cancerous liver tissue"
                            /clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: E
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced
Pieter de Jong"
145 c 133 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10116"
/clone="CH230-186C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
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69.5%;
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Pred. No. 2.4e-13;
                                                                                                                                                                                                                                                       Genome Center at Shanghai Zhangjiang Hi-Tech Park,
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                                                                                                                                                    Shanghai.
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GLCDHB01 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 ATCGGNGTTGGGCCAAGATCTCCAACATGACTTTTAGC 361
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BF724774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wistow,G.J., Bernstein,S., Behal,A. and Smith,D. NEIBANK: EST analysis and bioinformatics for ocula Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Section on Molecular Structure and Function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: graeme@helix.nih.gov
Plate: 08 row: e column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 598)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 402 3452
301 496 0078
                                      /note="Organ: Eye; vector: pcMvSpORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pcMvSpORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGCCCC(T)15-3'
]. Not I/Dlunt end inserts were cloned into the Not I/EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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/lab_host="SOLR"
\dot{\mathbf{V}} sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing
                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="bx08e07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Iris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.5%;
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Pred. No. 8.2e-11;
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RESULT 5
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182 GTGCCCACTATGCACCAGGCAATGTATATGATTCTAGAATTCAGCAACGAACAAGACAGA 123
                                                                                     349 GTATCTACAAGGCACCAGGCATTTTTGAGCATTTGGGGATTTGTCAGCAAACAAGTCAGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 AGTGTCTACTGTGTACTAGGGATTGTTCTAGCGGCTGGGATATAGCAGTAAACAAGGCAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GCAAAAATCCCTGACCTCATGGAACTGACCTTCTAG 1
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B92778 487 bp DNA linear GSS 25-JUN-1991
CIT-HSP-2164D13.TR CIT-HSP Homo sapiens genomic clone 2164D13, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
Other_GSSs: CIT-HSP-2164D13.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams, M.D., Rounsley, S.D., Zhao, S., Fisar, Wible, C., Shizuya, H., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simon, M. and Venter, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 487)
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a 142 c 146 g
                                                                                                                                                                                                                           HindIII"
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:7100687"
/db_xref="taxon:9606"
/clone="2164D13"
                                                                                                                                                                                                                                                                                                                                                                                         1. .487
                                                                                                                                                                                                                                                                                                   /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                               /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                /cell_type="Sperm"
                                                                                                                                                                                                                                                                                   /sex="Male"
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Pred. No. 0.011;
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                                                                                                                                                               DB 17;
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AUTHORS
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MEDLINE
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428 GGAGGGAACATTCTAGCAAAGGAA 451
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                                                                                                                                                                                Local Similarity
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C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., JT., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M.,

Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M.,

Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M.,

Fhillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Jumke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

Venter, T. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                         CATTITITGAGCATTIGGGATTIGTCAGCAAACAAGTCAGACAAAAAACCTIGCTCTGGT 427
                                            CTTGTTCTAGGCACTTGGGATTCACCAGTATACAATGGAGACAAAAATCCCCTGCCCTGGA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage, AR Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Index (http://www.tigr.org/tdb/hgi/hgi.html)
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EST42291 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                      /note="Organ: endometrium; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
78 c 104 g 83 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="ATCC (inhost):139297"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Endometrial tumor"
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                                                                                                                                                                          Score 44; DB 9;
Pred. No. 0.13;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                  DB 9;
                                                                                                                                                25; Indels
                                                                                                                                                                                               Length 372;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GCAGCTTACATTCTAGCATGGCAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 GGAGGGAACATTCTAGCAAAGGAA 451
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                      Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 407)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                    AQ085343
407 bp DNA linear GSS 26-AUG-19:
HS 2164_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=13 Row=D, DNA sequence.
                                                                    Sequence-tagged connectors: A sequence approach to mapping and
                                                            scanning the human genome
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                               Homo sapiens
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
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Plate: 224
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
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RESULT 9
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                                                                                                                                                                                                                                       - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                             project grant.
and Genevieve |
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f)
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
          /plasmid="pBeloBAC11"
/note="end : SP6"
63 c 75 g
                                                                           /clone_lib="DrosBAC"
                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                 Location/Qualifiers
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                                                                                                   /clone="BACN06M20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                            JOURNAL
                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CAGCAAACAAGTCAGACAAAAAACCTTGCTCTGGTGGAGGGAACATTCTAGCAAAGGAAG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 MMMMMMMMCACNAACAMMMMMMVGVMVMGGNNNNNTNNMNNNNGNNCTTNTCNTNTN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTTMTNTNTNMMCTNTCCMMMNMNNNTMNNNNMMNMNNNNNNNMMNNTNNNNNNN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNNAMAMMTTMMMANNNNMMNTNNNMNMNGNNNGGTTKMGKGKGMGGMCNMTTTMM 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAATGACAAGCAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGGAAGAGATGAGTTT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGGCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATTTGAGAATCATTCACTGAGCA 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTGMGTMTTNGTTMTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGTGAGAGCAGGGAGTGCGTGCTGGGCTGAGGAACCAGAGGTAATGGCCCCTGGGGACGC 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt MMNMMMNNNMGGKGTTKMMMYMGMGGMKGKMGKHKKMGMGVGKGTKMTMCGGMMGKG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNMTNMNNNMNNMNNMNNNNNNNNNNNNNTTTTTTTMMCTTHMTHMTMTHMMTTTHMTM 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMT NNT MMMNNT NNNNMMMMMMMMNT MMNMNMMMMMT CNMNMMT MMT MNG MNMNMG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMSSGGMMGMMVGGSGGVSGCGGVMGGGGKSGGMMKKMKGYGTMMGGMVGGGGGGGBMGM 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAACTATGTAACCAGCATTGGGTTGGGTGCCAGAGATCCAAAGCTAAGACACCAAAACC 812
                                                                                                                                         Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                        BG197160
RST16397
Email: scain@athersys.com
                   3201 Carnegie Ave,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                    1 (bases 1 to 198)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D.,
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                        Athersys,
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        BG197160.1
                                                                                                                                                                                                                                                                                                                                                                                                           BG197160
                                                                                                                                                                                                                                                                                                                                                    human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 148; Mismatches
                                                                                                                            Biotechnol. 19 (5),
                                                                                                                                                                                                                                                                                                                                                                                                                          Athersys RAGE Library
                                                                        Inc.
                                                                                                                                                                                                                                                                                                                                                                                        GI:13718847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807
                                                       Cleveland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.6; DB Pred. No. 0.23;
                                                                                                                              440-445
                                                                                                                                                                                                                                                                                                                                                                                                                                             198
                                                                                                                                                                                                                                                                                                                                                                                                                                           đđ
                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                       44115,
                                                                                                                              (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                          Perry, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2001
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FEATURES

High

source

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465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
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                                                                                                                                                                                                                                                      High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Tel: (206) 616-3887
Email: ywallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                             http://www.htsc.washington.edu
Plate: 957 row: K column: 1
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ669724 438 bp DNA linear GSS 24-JUN-1999 HS_5381_A1_F01_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=957 Col=1 Row-K, DNA sequence. AQ669724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                    quality sequence stop: 438
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 148.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                         /db_xref="taxon:9606"
/clone="Plate=957 Col=1 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.4; DB Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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SOURCE
ORGANISM
    Db
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AQ013160
LOCUS
                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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Best Local S
Matches 59
                                                                                                           Query Match
Best Local 9
                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                           source
                             163 CCAGATATATTGTAGGCACTGAGGATATAGTGGTGAACAAAACAGGTGATCATCCTTGCC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGTGGAGCTTACATTCTAAAATA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGTGGAGGGAACATTCTAGCAAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCATTATTCTAGGCACTTGGGATATATCAGTGAACAAAACAGACAAAAATCCCTGTC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGCATTTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAACCTTGCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are availabe from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ013160 355 bp DNA linear GSS Ub-JUN-1: CIT-HSP-2298M3.TF CIT-HSP Homo sapiens genomic clone 2298M3, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ013160.1 GI:3185725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 355)
                                                                                                                                                                                                    113
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301 838 0200
301 838 0208
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                             /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
67 c 83 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen dc and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

87 c 62 g 122 t 1 others
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="2298M3"
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:7153855"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa;
                                                                                                           3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                      0;
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                                                                                                         Score 43.2; DB Pred. No. 0.22;
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                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MD 20850,
                                                                                      48;
                                                                                                                             17;
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RESULT 11 AQ669724

DEFINITION

VERSION

AQ669724.1 GI:5202558

SOURCE KEYWORDS ACCESSION

ORGANISM

Homo sapiens Eukaryota; M

δÃ В Š

525

90

TTAATGCCACCGACATCCCATGTGG 56 TTAATACCATCAATATCCCATGAGG 549 ORIGIN BASE COUNT

55

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Matches Query Match

Conservative

0;

3.7%; 69.4%;

Best Local Similarity

REFERENCE AUTHORS

COMMENT

JOURNAL MEDLINE TITLE

Proc.

scanning the human genome

FEATURES

source

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RESULT 13
BG940945
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Best Local
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TITLE
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381 TTTGGGATTTGTCAGCAAACAAGTCAGACAAAAAAACCTTGCTCTGGTGGAGGGAACATTC 440
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                                                                              Local Similarity les 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGGAGGGAACATTCTAGCAAAGGAAGGCAAATGACAAGCAGGAGAAGTATTTGCTA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 384)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG940945

384 bp mRNA linear EST 11-JUN-: ax08d07.x2 Proliferating Human Erythroid Cells (LCB:ax library) Homo sapiens cDNA clone ax08d07 random, mRNA sequence. BG940945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intramural Sequencing Center (NISC).
Plate: 08 row: d column: 07
Seq primer: -21M13 forward primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 402 2373
Fax: 301 435 5148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jm7f@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG940945.1 GI:14340317
                                                                                                                                                                                                            152
                                                                                 Conservative
                                                                                                                                                                                            Site_2: ECORI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using TRTzol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's Capfinder CDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcorI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
http://www.nisc.nih.gov/)."
52 a 48 c 73 g 111 t
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/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="ax08d07"
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                                                                                                      3.7%;
62.0%;
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                                                                                                      Pred. No. 0.39;
                                                                                                                           Score 42.4; DB 13;
                                                                           Mismatches
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                                    465
                                                                            254
                                                                                                                   405
                                                                                                                                                          194 CGAGCACTTACTGTACACCAGGCATTGTTCTAGGTATATGAGATTCATTAACAAACTAAA 253
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314 TAATAAATATACTACATTAGAA 335
                                                                                                                                                                                          346 CAAGTATCTACAAGGCACCAGGCATT-TTTTGAGCATTTGGGGATTTGTCAGCAAACAAGT 404
                                                                                                                                                                                                                                                        Local Similarity
                                                                                            CAGGAGAAGTATTTGCTAAGAA 486
                                                                         TAGCAAAGGAAAGCAAATGACAAGCAGGAGAAGTATTTGCTAAGAATG 488
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                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AG154770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-018005.TJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes DNA, clone: RP43-018005.TJ, genomic survey
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                                                                                                                                                                                                                                    Conservative
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R.Site 2 : ECORI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tracking errors.
                                                                                                                                                                                                                                                                                                                                /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
192 c 79 g 206 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP43-018005.TJ"
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60.6%;
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RESULT 15 BG203357/c

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REFERENCE
AUTHORS
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ORIGIN
Search completed: December 8, 2002, 19:26:54
Job time: 2585.48 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                        525 TTAATACCATCAATATCCCATGAGG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pact 1. Cain
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Emall: scain@athersys.com
Emall: scain@athersys.com
Location/Qualifiers
1. Capienes 276.
276
                                                                                                                                                                               31
                                                                                                                                                                               TTAATGCCACCGACATCCCATCTGG
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Homo Sapiens
Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Eŭteleostomi;
Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 276)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Harrington,J.J., Sherf,B., Thornton,M., Ramachandran,R., Whittington,
Proventhal,C., Thornton,M., Ramachandran,R., Ways,R., Smit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

activation of gene expression

Mat. Biotechnol. 19 (5), 440-445 (2001)
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BG203357
BG203357.1
GI:13725044
BG203357.1
BG20357.1
BG20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 51 c 59 g 74 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 0.52;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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1161
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23: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: *
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25: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: *
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Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (without alignments)
7908.746 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

9	8	7	6	տ	4	ω	2	1	No.	Result
126	126	126	126	126	126	126	126.2	268	Score	
10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	23.1	Match !	Query
1945	954	954	954	954	954	954	741	1186	Length	
24	22	22	22	19	19	19	19	24	DB	
ABK12877	AAD05904	AAD08715	AAD15311	AAV41372	AAV41378	AAV69887	AAV69899	ABK33576	ID	
cDNA encoding huma	Human full-length	Human receptor act	Human receptor act	NF-kB receptor act	NF-kB receptor act	Nucleic acid encod	Nucleic acid encod	cDNA encoding huma	Description	

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659 983	1001	519	546	564	564	519	519	519	2029	522	2299	2295	2237	2237	2191	1630	1630	1630	1630	1630	1574	1538	951	951	951	951	735	957	1823	2390	2274	2271	2226
222	21	21	21	21	21	21	21	21	21	22	21	19	24	20	19	22	22	22	19	19	22	19	21	21	21	19	19	22	20	24	19	21	24
AAL00215 AAH34950	AAH51392 AAH51308	AAZ99973	AA299971	AAZ99970	AAZ99967	AAZ99972	AAZ99969	AAZ99968	AAA39155	AAS13369	AAZ99966	AAV70284	ABK12880	AAX80224	AAV41489	AAD05903	AAD08714	AAD15310	AAV41371	AAV41377	AAH25526	AAV69886	AAZ49024	AAZ99965	AAA39156	AAV69900	AAV69898	AAF86481	AAX80223	ABK40274	AAV70285	σ	ABK12876
repro	Human GLCL related	ncodin	DNA encoding osteo	ő		DNA encoding osteo	D	DNA encoding a syn	Mouse OBM nucleoti	Mouse cDNA encodin	DNA encoding a mur	Human osteoprotege	cDNA encoding mous	Murine TRANCE enco	Nucleotide sequenc	Murine RANKL (rece	Murine receptor ac	Murine receptor ac	NF-kB receptor act	NF-kB receptor act	Nucleotide sequenc	Nucleic acid encod	Osteoclast formati	DNA encoding a mur	Mouse OBM nucleoti	Nucleotide sequenc	Nucleic acid encod	Rat osteoclast dif		cDNA encoding huma	rot	encoding a	cDNA encoding huma

ALIGNMENTS

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25-JUL-2000; 2000US-220866P. 26-JUL-2000; 2000US-220893P.					25-JUL-2000; 2000US-220605P.				29-JUN-2001; 2001WO-US21066.		31-JAN-2002.		WO200208288-A2.		Homo sapiens.		tumour necrosis factor-alpha; gene; ss.	pericyte cell proliferation; chondrocyte cell proliferation;	breast cancer; prostate tumour; rectal tumour; liver tumour;	Human; secreted protein; PRO; tumour; lung cancer; colon cancer;		cDNA encoding human PRO protein, Seq ID No 81.		08-MAY-2002 (first entry)		ABK33576;	ABK33576 standard; cDNA; 1186 BP.		LT 1

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Best Local
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28-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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23-AUG-2000;
24-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
                                                                                                          490
                                                                                                                                                                                                               Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2001;
10-MAY-2001;
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670
                                    610
                                                     649
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                                                                                                                            529
                                                                                                                                             430
                                                                                                                                                    469 AGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAA 528
                                                                                                                ATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTT
                                                                                                        AGGACCTTCAGCTATGGTGTAATTTGAG
                 AGGACCTTCAGCTATGGTGTAATTTGAG 736
                                  ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC
                                                  ATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGC
                                                                     ATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTT
                                                                                                                                          AGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAA 489
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DB; AAU83632.
                                                                                                                                                                                268;
                                                                                                                                                                                                                                                                                                                                                                                    2; Figure 81; 359pp; English.
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                         liver tumour
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C, Gurney
                                                                                                                                                                                Conservative
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2001WO-US06520.
2001US-0854280.
2001WO-US17092.
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2000WO-US23522
2000WO-US23328
2000US-000000P
2000WO-US30873
2000WO-US3646P
2000WO-US36678
2000WO-US32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL,
                                                                                                                                                                                     100.0%;
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Smith V,
                                                                                                                                                                               0;
                                                                                                                                                                               Mismatches
697
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Stephan
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                                                                                                                                                                                               Length
                                                                                                                                                                               Indels
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                                                                                                                                                                                                1186;
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RESULT

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Best Local
                                                                                                        Matches
                                                                                                                                                                                                                   (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of Osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PFH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein for investigative and disposetic substances.
                                                                                                                                                                                                          of the protein,
                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the
                                                                                                                                                                                                                                                                                                                                                                                                                                               for, e.g. treatment calcium metabolism
                                                                                                                                                               Sequence 741 BP; 230 A; 153 C; 158 G;
                                                                                                                                                                                             components of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
465 -CAGGAGAAGTATITTGCTAAGAATGGCAATCCTGACGCTCCAGCCTTCAACTCATCTTGTT 523
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1997;
12-AUG-1997;
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15-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
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                                                                        GAATTACAACATATCGTTGGATCACAGCACATCAGAGCAGAGAAAGCGATGGTGCATGGC 234
                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N, Shima N,
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Pages 121-122; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding a human OCIF-binding molecule
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97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
                                                                                                                                                                                                        for investigative and diagnostic purposes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-JP01728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  absorption factor; bone disorder; calcium metabolism;
                                                                                                                      10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinosaki M, I
Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ผ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yano K,
                                                                                                        0
                                                                                                                    Score 126.2; DB 1
Pred. No. 3.8e-30;
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kobayashi F,
, Tomoyasu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yasuda H;
                                                                                                                                                               200 T; 0 other;
                                                                                                                                  DB 19;
                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morinaga ?
Tsuda E;
                                                                                                       Indels
                                                                                                                                  Length
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The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane protein then affinity chromatography using OCIF. It exists in a full-sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV69887 standard; cDNA to mRNA;
                                                                                                                                                                                                                                 Nakagawa N, Surmaguchi
                                                                                                                                                                                                                                                                                                                                           09-JUN-1997;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; ss.
                                                                                                                                                       Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9846644-A1
                                                                                                                 Claim 38; Page 115; 151pp; Japanese
                                                                                                                                             calcium metabolism
                                                                                                                                                                                                                 WPI; 1998-594563/50.
                                                                                                                                                                                                                                                                                                 (SNOW ) SNOW BRAND MILK PROD CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCAAGATTGGGCAAACGTCTCCAACATGACTTCAGCAACGGAAAACTAAGAGTCA - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACAT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCA 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCAT
                                                                                                                                                                                                                                                        Higashio K,
N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a human OCIF-binding molecule (OBM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                            97JP-0332241.
97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1..954
                                                                                                                                                                                                                                                                       Kinosaki M,
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K, Yano K, Yasuda H;
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                                                                                                                                                                                                                                                          Morinaga '
                   membrane proteins
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AAV41378
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Best Local
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                                                                                                   14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    components of drugs.
                                                                                                                                                                                                                                                                                                                            RANKL; RANK ligand; tumour necrosis factor; TNF; ss
                                                                                                                                                                                                                                                                                                                                                                           NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV41378 standard; cDNA; 954
             P-PSDB; AAW69957
                                                                                                                                                                               02-JUL-1998.
                                                                                                                                                                                                         W09828426-A2
                                                                                                                                                                                                                                                                                                  Homo sapiens
                        WPI; 1998-377657/32
                                                  Anderson DM,
                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                       22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTAACTCTGCAGGACCTTCAGCTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                   necrosis factor-kappa B; NF-kB; receptor activator; human;
                                                                                                                                                                                                                                                                                                                                      response;
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                                                  Galibert
                                                                                                   97US-0064671.
96US-0059978.
97US-0813509.
                                                                                                                                                       97WO-US23775
                                                                                                                                                                                                                                /*tag= a
/product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.9%;
                                                  ĽJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                  Maraskovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                  E
                                                                                                                                                                                                                                                                                                                                           toxic shock; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19;
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RESULT 5
AAV41372
ID AAV4
AX AAV4
AC AAV4
XX DT 08-0
DT 08-0
CX RANK
KW RANK
KW Immu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This cDNA encodes a human RANKL, a ligand for the RANK (receptor CC activator of necrosis factor-kappab (NF-kB)) polypeptide. RANK is a activator of necrosis factor (TNF) amply amply a soluble RANK (CC may be used for inhibiting activation of NF-kB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CRANK ligand (RANKL). RANKL polypeptides can activate RANK and can be CC used to induce maturation of dendritic cells and enhance their CC soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists CC may be useful in ameliorating negative effects of an inflammatory capacity. The composition may also be used for regulating an immune or inflammatory response. Inhibition, or acute inflammatory capacity response that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic reactions. They can also be used in adjunct therapy for disease contacterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of from the negative effects of chemotherapy or the presence of high levels contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                        RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                                           NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                     AAV41372 standard; cDNA; 954 BP
                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                  08-OCT-1998
                                                                                                                                                                                                                                                                                                              AAV41372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
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                                                                                                                                                                                                                                                             (first entry)
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%;
72.6%;
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Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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AAD15311 standard; cDNA; 954 BP

AAD15311;

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RESULT 6
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                                                                                                                                                                                                                                                                                                                             δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                   δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in inflammatory reactions. They can also be used in adjunct therapy for classes characterised by neoplastic cells that express RANK. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                                                     569
                                                                                                                                                                                                                                                         583
                                                                                                                                                                                                                                                                                             509
                                                                                                                                                                                                                                                                                                                                                                     449
                                                                                                                                                                                                                                                                                                                                                                                               465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated receptor activator of necrosis factor-kappa of information of necrosis factor-kappa of for e.g. developing products for regulating an immune or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-377655/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9828424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1998.
                                                                                                                                                                                                                                ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                                                                                           CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                     ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                      GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                           AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                     TTAATGCCACCGACATCCCATCTGGTTCCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                       TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                             ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                              ATCGGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galibert LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0064671.
96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.9%;
72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 126; DB 19;
Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                             696
                                                                                                                                                                                                                                                   639
                                                                                                                                         889
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CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member CC of the tumour necrosis factor (TNF) receptor superfamily and associates CC with TNF receptor associated factor (TRAF) 2 and 3 which are important CC in the regulation of immune and inflammatory response. The receptors of immune and inflammatory response. The receptors CC are useful for regulating immune response and in screening for inhibitors CC of these receptors. The cytoplasmic domain of RANK is used in developing CC assays for inhibitors of signal transduction, e.g. for screening the molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, CC TRAF5 and particularly TRAF6. NF kappaB inhibition by RANK antagonists CC are useful in ameliorating the negative effects of an inflammatory CC response that result from triggering of RANK, e.g. in treating toxic consolved the effects of bone rescription. RANK acts as an anti-cc apoptotic signal and rescue the cells that express RANK from apoptosis. CC soluble forms of the receptor are used in vivo or in vitro based CC screening tests for agonists or antagonists of RANK mediated NF kappa B activation, or to inhibit transduction of a signal via RANK. RANK compositions are used in the CC development of both agonistic and antagonistic antibodies, or as an acc adjunct therapy for disease characterised by neoplastic cells that cc are useful for modulating the formation of osteoclasts from osteoclast form osteoclast find screening the inhibitors of diseases associated with RANK/TRAF6 interactions and inhibitors of diseases associated with RANK compositions. They care used in which it is a member of the receptor as associated with RANK compositions. They care used in highlitors of diseases associated with RANK compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-520313/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougall WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Column 69-71; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ( VMMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1997;
are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patent discloses novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor activator of NF kappaB ligand (RANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE08738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galibert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0064671.
96US-0772330.
97US-0813509.
97US-0996139.
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97US-0077181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human RANK ligand (RANKL) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor activator of nuclear factor (NF)-
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RESULT 7
AAD08715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
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Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is a cDNA enco human RANK ligand (RANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human receptor activator of NF-chi B ligand (huRANKL) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD08715 standard; cDNA; 954 BP
                                                                    WPI; 2001-407216/43.
P-PSDB; AAE04426.
                                                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                  23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                    US6242213-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                    14-OCT-1997;
                                                                                                                                                                                                                           22-DEC-1997;
                                                                                                                                                                                                                                                        05-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                               DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                   96US-0059978.
97US-0077181.
97US-0064671.
                                                                                                                                                                                                                             97US-0995659
                                                                                                                                                                                                                                                                                                               /product= "Human RANKL protein"
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 126; DB 22; Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         889
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New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK) -

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AADOS904
ID AADO
XX
AC AADO
XX
AC AADO
XX
31-C
XX
Huma
KW Huma
KW Inf:
KW Inf:
KW Es:
XW Es:

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17-NOV-1999;
                                                            14-NOV-2000; 2000WO-US31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; receptor activator of NF-kappaB; RANK; nuclear factor-KappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
                                                                                                                                                                                                   WO200136637-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF receptor-associated factor; TRAF; RANK ligand; RANKL; Osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD05904 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Column 61-64; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         689 ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAF3. The DNA molecules are useful for producing ligands of RANK. Ligands are useful for regulating immune response and in screening inhibitors of RANK. The present sequence is human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
   99US-0442029
                                                                                                                                                                                                                                            /product= "Human full-length RANKL (receptor activator of NF-kappaB ligand) protein"
                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126; DB 22; Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
           Human; tumour necrosis factor-related activation induced cytokine;
                                                    cDNA encoding human TRANCE protein splice variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The present sequence is a cDNA encoding full-length human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factors (TRAFs). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANK) results in upregulation of the transcription factor NF-KappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-KappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in Gene +hereny analogues in infecting target
                                                                                                   18-JUN-2002 (first entry)
                                                                                                                                                                                       ABK12877 standard; cDNA; 1945 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a novel receptor, referred to as (receptor activator of NF (nuclear factor) *RappaB), a member of TN (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor associated
                                                                                                                                                                                                                                                                                                        689
                                                                                                                                                                                                                                                                                                                                                                                         629
                                                                                                                                                                                                                                                                                                                                                                                                                                  640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 75-76; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson DM, Hughes AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                          GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                                                                                                                                                                                                                                                 ACCTAGCTACAGAGTATCTTCAACTA 714
                                                                                                                                                                                                                                                                                                                                                                                  AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                           ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RANKL gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126; DB 22;
Pred. No. 5.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                  688
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TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;

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                                                                                                                                                                                                              cc having a disorder comprising insufficient or excessive cartilage or comprising insufficient or excessive cartilage or cc skeletal growth. The method of the invention involves administering to cc the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE ) modulating agent. The method is useful for treating a mammal cc having a disorder comprising insufficient or excessive cartilage or complete the disorder comprising insufficient cartilage or cskeletal growth where the disorder comprising insufficient cartilage or cc resulting from traumatic injury, surgery, osteopetrosis, cranitofacial-skeletal discrepancies and bone or cartilage damage cc resulting from traumatic injury, surgery, osteopetrosis, or heumatic crawthitis, and disorders comprising excessive cartilage or skeletal cc growth are selected from acromegaly, gigantism, exostosis, carilaginea, cc exostosis bursata and multiple osteocartilaginous exostoses. The method concluded acid sequence encodes the human TRANCE protein, splice variant cc family and acts directly on cartilage-producing cells (chondrocytes).
                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte; cartilage growth; skeletal growth; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200216551-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-2000; 2000US-226197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001; 2001WO-US26101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating mammal having disorder characterised by abnorma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU78286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT
                                                                                                                                                                                     Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new method of treating a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 55pp; English.
                                      324
 525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
                                                                         465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                  Similarity
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95..829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note- "Target region for antisense nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Tumour necrosis factor (ligand) superfamily,
    member 11 (TNFSF11), Specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                               10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation induced cytokine) protein splice variant 2"
                                                                                                                             Score 126; DB 24; Length 1945; Pred. No. 7.7e-30;
                                                                                                               Mismatches
                                                                                                                 65;
                                                                                                                 Indels
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ABK12876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis; rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea; exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK12876 standard; cDNA; 2226 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding human TRANCE protein splice variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cartilage growth; skeletal growth; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                      18-AUG-2000; 2000US-226197P
                                                                                                                                                                                                                                                                20-AUG-2001; 2001WO-US26101
                                                                                                                                                                                                                                                                                                                 WO200216551-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 ACCTAGCTACAGAGTATCTTCAACTA 589
                                                           Disclosure; Fig 1; 55pp; English.
                                                                                                                         Treating mammal having disorder characterised by abnormal
                                                                                                                                                   P-PSDB; AAU78285.
                                                                                                                                                                                                              (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                               2002-304119/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour necrosis factor-related activation induced cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Tumour necrosis factor (ligand) superfamily,
    member 11 (TNFSF11), target region for antisense
    nucleic acid. Specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                /product= "Human TRANCE (tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                          157..1110
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                         Marks SC;
                                                                                                                                                                                                                                                                                                                                           splice variant 1"
                                                                                                                                                                                                                                                                                                                                                       activation induced cytokine)
                                                                                                                                                                                                                                                                                                                                                        protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443
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The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering

a tumour necrosis factor-related activation induced

cytokine

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mammal

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ID AAZS
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AC AAZS
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DX 25-:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
(MEBI-) M & E
                                                                       15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                         13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                   WO200015807-A1
                                                                                                                                                                                                                                      23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ99964 standard; DNA; 2271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA--- 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCGTTGGAAACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and acts directly on cartilage-producing cells (chondrocytes).
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Similarity 72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
      BIOTECH AS
                                                                   98DK-0001164.
98US-0102896.
                                                                                                                                                                  99WO-DK00481.
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 185..1138
                                                                                                                                                                                                                                                                                                                                                   /product= "osteoprotegerin ligand"
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis; bone resorption; ss
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Pred. No. 8.3e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                   Homo sapiens
                                                                                                                                  Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
                                                                                                                                                                                      Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                         Paget's disease;
                                                                                                                 hypercalcaemia; osteoclast differentiation and activation receptor
                                                                                                                                                                                                                                   11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                          AAV70285 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein. The murine and human OPGL polypeptides are 87% homologous a potent osteoclast differentiation factor when combined with
                                                                                                                                                                                                                                                                                                                                                                                                                        697 GCCTAACTCTGCAGGACCTTCAGCTA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halkier T, Haaning
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                                                                                                                                                                                                                                                                                                                                                                                                     ACCTAGCTACAGAGTATCTTCAACTA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTCGAAACATG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193;
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72.6%;
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Pred. No. 8.4e-30;
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Location/Qualifiers 185..1138

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotein. OPG binding protein is used in binding assays to determine osteoproteins: (OC) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1998;
16-APR-1997;
23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boyle WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes human osteoprotegerin (OPG) binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9846751-A1
                                                                                                                                                                                                                                                                                                                                     Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses,
                                                                                                                                                                                                                                                                                                                                                              optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                        465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                      525 TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTCTTGGAAACATG 582
            873
                                    697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                   753
                                                                                                                                                                        693 TTAATGCCACCGACATCCCGTCTGGTTCCCATAAAGTGAGTCTGTCCTTCTTGGTACCATG
                                                                                                                                                                                                                             CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells transfected with vectors containing nucleic acid molecules
            ACCTAGCTACAGAGTATCTTCAACTA 898
                                                               AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                             ---AAGGCATTTATTACCGGAAITGCCGACAITTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                   ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                             ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                193;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0052521.
97US-0842842.
97US-0880855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US07584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "osteoprotegerin binding protein"
                                                                                                                                                                                                                                                                                           10.9%;
72.6%;
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                            Score 126; DB 19, Pred. No. 8.4e-30
                                                                                                                                                                                                                                                                                                         DB 19; Length 2274;
                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                             639
                                                                                                                                                                        752
                                                               872
                                                                                                                   812
                                                                                                                                                                                                                                                                                2
                                                  ABK40274
Matches
           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          WPI;
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02-JUN-1999;
22-JUN-1999;
22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999;
11-MAR-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-1999;
01-SEP-1999;
15-SEP-1999;
                                                                                                                                             polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc.) leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic discinflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK40274 standard; cDNA; 2390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding human PRO206 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 50; Fig 41; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignancies, inflammatory, angiogenic and immunologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAU86148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                           Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi AJ,
                                                                                                                             polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-205567/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan J, I
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-146222P.
99US-149395P.
99US-151689P.
99WO-US20111.
99WO-US21090.
99WO-US21313.
99WO-US28301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-145698P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-144758P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-140650P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US12252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-123972P
99US-133459P
10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski PJ,
Score 126; DB 24; Pred. No. 8.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney AL,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     blastocoelic disorder;
                      Length 2390;
```

Qy

Similarity

Conservative

0;

Mismatches

Indels

,. &

Gaps

465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524

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RESULT 14
AAX80223
ID AAX80
AC AAX80
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
cytckines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1998;
12-DEC-1997;
03-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNF like proteins for treating autoimmunity and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                                                                                                                                                                                                                                                                                                                                        The present sequence encodes human TNF-related activation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TRANCE encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9929865-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX80223 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-385609/32.
DB; AAY17873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTAGCTACAGAGTATCTTCAACTA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Josien R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0989479.
97US-0989479.
98US-0034099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US26486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steinman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1823 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Won
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          813
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AAF86481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SXCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
The present sequence is the coding sequence for Differentiation Factor (ODF). ODF is thought to
                                        Claim 1;
                                                                      Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation,
                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                               P-PSDB; AAB82092
                                                                                                                                                   Xu J,
                                                                                                                                                                         (UYWA-) UNIV WESTERN AUSTRALIA
                                                                                                                                                                                                  29-SEP-1999;
                                                                                                                                                                                                                         29-SEP-2000;
                                                                                                                                                                                                                                                 05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                 Osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                Rat osteoclast differentiation factor, ODF, coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF86481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF86481 standard; cDNA; 957
                                                                                                                                                                                                                                                                       WO200123549-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1823 BP; 569 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          697 GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 292
                                                                differentiation
                                                                                                                                                                                                                                                                                                                                                                               osteoclast formation inducer; vaccine; oclast Differentiation Factor; bone; ss.
                                                                                                                           2001-335526/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAATGCCACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTCTTGGTACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAATACCATCAATATCCCATGAGGCT--CATAAAACGAGTCTTTCTTGCTTGGAAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTAGCTACAGAGTATCTTCAACTA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCGGGGGTGGGGTAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
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TITLE The sequ	AUTHORS Waterston, R.H.	REFERENCE 1 (base	Mammalia	Eukaryota	ORGANISM Homo sapiens	SOURCE Homo sapiens	KEYWORDS HTG; HTG:	VERSION AC104794	ACCESSION AC104794	3 unordes	DEFINITION Homo sap	LOCUS AC104794	AC104794	KESOLI I
The sequence of Homo sapiens Clone	n,R.H.	1 (bases 1 to 165707)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Verlebiata; Eucereoscomit,	iens	iens.	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.	AC104794.3 GI:20340520		3 unordered pieces.	Homo sapiens chromosome 2 clone RPII-254F/, WURNING DRAFI SERGENCE,	ACCOUNTS OF THE TENT OF THE TE		

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                                                                                                            Matches 468;
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40150 AAAAGAGGATAATTCAAGAAGGGCTTCTTTAAGGGACTATTTCCCAAGATGGGAATGGAG 40209
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Sequencing vector: plasmid; 1008
Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162662 bases at least 040
Consensus quality: 163189 bases at least 030
Consensus quality: 164786 bases at least 020
Insert size: 9479; agarose-fp
Insert size: 167795; sum-of-contigs
Quality coverage: 12.78 in 020 bases; sum-of-contigs
Quality coverage: 10.53 in 020 bases; sum-of-contigs
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76328. .165707
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42887 a 42242 c 39083 g 41295 t
                                                                                                                             Similarity
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Submitted (30-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On APR 30, 2002 this sequence version replaced gi:19339129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Project Information ------
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Submitted (21-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
                                                                                                         Conservative
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76228
76328
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1213. .76227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1112: contig of 1112 bp in length
1212: gap of unknown length
76227: contig of 75015 bp in length
76327: gap of unknown length
165707: contig of 89380 bp in length
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                                                                                                                 Score 467.4; DB 2; Length 165707; Pred. No. 5.3e-134;
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 Submitted (07-NOV-2001) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                 Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                        Direct Submission
Submitted (19-APR-2001) Genome
University School of Medicine,
                                       Direct Submission
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Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                            Waterston, R.
                                                                                             MO 63108,
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The sequence of Homo sapiens BAC clone RP11-95D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 190748)
Sulston, J. E. and Waterston, R.
Toward a Complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Homo sapiens BAC clone RP11-95D17 from 2, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Apr 19, 2001 this sequence version replaced gi:11128441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP11-521D12. Actual start this clone is at base position 1 of RP11-95D17; actual end is base position 190748 of RP11-95D17.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unresolved tandem repeat from base position 181200 to 187300. Si information from restriction digest suggests that the full repeat may not be represented.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEIGHBORING SEQUENCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sapiens@watson.wustl.edu
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                    /rpt_family="L2" 3716. .3745
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806. .1114
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/db_xref="taxon:9606"
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                                                                                                /rpt_family="MIR" 2179. .2369
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325. .805
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/rpt_family="AT_rich"
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9652. .9784
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8242. .8532
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              /note="similar to 13729, .14126 /note="similar to 13735, .13801
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11135. .11420
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13727. .14127
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12955. .13065
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12698. .12954
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12467. .12594
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12335. .12416
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13623. .14122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 40.3%; Score 467.4; DB 9; Length 190748; Local Similarity 99.8%; Pred. No. 5.4e-134;
                                                                                                              Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., GodowsKi,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.
                                                          Genentech Inc. (US)
                                                                                            Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                         Patent: WO 0193983-A 81 13-DEC-2001;
                                                                                          the same
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                Sequence 81 from Patent W00193983. 
AX358828
                                                                                                                                                                                                                                                 AX358828.1 GI:18675315
                                                                                                                                                                                                                                                                                             AX358828
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                 Location/Qualifiers
1. .1186
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14144. .14259
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14422. .14474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 23.1%; Score 268; DB 6; Length 1186; Local Similarity 100.0%; Pred. No. 5.9e-72; hes 268; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                      268;
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                                                                                                                                                                                                                                                                                                                                                                                           Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.
                                                                                                                                                                                                                                                                                                                                                    Genentech,
                                                                                                                                                                                                                                                                                                                                                              Patent: WO 0208288-A 81 31-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                               Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                  Dodge, S., Domino, M., Doyle, M., Ferreita, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Iliev, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Lancoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfâye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Young, G., Zalnoun, J., Zimmer, A., and Zody, M.
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Homo sapiens chromosome 2 clone RP11-164P8 map 2, WORKING DRAFT
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Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Oct 4, 2000 this sequence version replaced gi:7331634. All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                                                                                                                                                                                                                  Zimmer, A. and Zody, M.
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FEATURES
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * consists of 21 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 144198 bases at least Q40 consensus quality: 151395 bases at least Q30 consensus quality: 153976 bases at least Q30 remains quality: 153976 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 155250; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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82120 107411
107412 107511:
107512 116168
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12626 12725: gap of 100 bp in length

12726 15710: contry of 2985 bp in length

15711 15810: gap of 100 bp

15811 19721: contry of 3911 bp in length

19722 19821: gap of 100 bp

19822 24311: contry of 4490 bp in length

19822 24311: contry of 4490 bp in length
                           146713 146812: gap of 100 bp
146813 157250: contig of 10438 bp in length
                                                                       107412 107511: gap of 100 bp 107512 116168: contig of 8657 bp in length 116169 116268: gap of 100 bp 116169 116269 128458: gap of 100 bp 128459 128558: gap of 100 bp 100 bp 1005128559 146712: contig of 18154 bp in length
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64505 71871: contig of 7367 bp in length
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6137: contig of 2088 bp in length

6138 6237: gap of 100 bp

6238 8049: contig of 1812 bp in length

8050 8149: gap of 100 bp

8150 12625: contig of 4476 bp in length
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Location/Qualifiers
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40400; contig of 7625 bp
0500; gap of 100 bp
47416; contig of 6916 bp
                                                                                                                                                                                                                             971: gap of 100 bp
82019: contig of 10048 bp in length
1119: gap of 100 bp
107411: contig of 25292 bp in length
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64404: contig of 7561 bp in length
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8: gap of 100 bp
3949; contig of 1561 bp in length
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0: gap of 100 bp
2288: contig of 1288 bp in length
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source

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Db 149245 CTGAAGTTGTAACTCTGAACCACAGGACAAGCATGATGTGATGTCTTCCTCACTAAATG 149186
                                                                                                                                                 Db 149305 GTTATGTTTGATTTCATAGGGATTTGCATTTGTGGATGAACTTGTGTGTTCACCTGAAGG 149246
                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                          Query Match
               1122 ATATGCTTATCGCATGCTTTTAATAAAAGGAGGAAAATGC 1161
                                                                 1062 GCAATGTCCTTGAGAAGACCCTGTCTTAATCATCTCTGTGTCTCACGCCTGGCTCATAAC 1121
                                                                                                          misc_feature
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47517. .56743
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146813. .157250
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128559. .146712
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32776 40400
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/db_xref="taxon:9606"
/chromosome="2"
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95.5%;
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                                                                                                                                                                                                                     Score 204; DB 2;
Pred. No. 9.8e-52;
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AB064268
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553 ACCTAGCTACAGAGTATCTTCAACTA 578
                                                                           493 AGGATGGCTTTTATTACCTGTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAG
                                                                                                 640 ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG
                                                                                                                                                             433 ATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATC
                                                                                                                                                                                                                                                                                                                                                                      465 CAGGAGAAGTATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTA 524
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                                                                                                                                                                                                                                                                                                                                313 CATGGTTAGATCTGGCCAAGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTA 372
                                       GCCTAACTCTGCAGGACCTTCAGCTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ikeda, T. and Kuroya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ikeda,T., Kuroyama,H. and Hirokawa,K.
Determination of human RANKL isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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RIKQAFQCAVQKELQHIYGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDI
PSGSHKYGLSSMYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLAT
EYLQLMVYYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
EYSNPSLLDPDQDATYFGAFKYRDID"
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/db_xref="GI:18143617"
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ligand 3"
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Pred. No. 1.3e-27;
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                                                                                                                                                                                                                                                                                                        ---AAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAG 696
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Homo sapiens male tongue epithelial-like squamous cell cacinoma cell_line:SCC-4 cDNA to mRNA.
                                                                         Homo sapiens mRNA for sODF/TRANCE, AB037599
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Homo sapiens mRNA for hRANKL
AB061227
                                                      AB037599.1 GI:6863047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                             AB037599
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/protein_id="bab71768.1"
/protein_id="Bab71768.1"
/db_xref="GI:16610213"
/db_xref="GI:16610213"
/translation="mFVALLGLIGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL
RLHENADFQDTTLESQDTKLLFDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG
SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLI
VNQDGFYYLYANICFRHHETSGDLATEYLQLAVYYVTKTSIKIPSSHTLMKGGSTKYWS
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AR156434.1
                      Sequence 12 from patent US 6242213. AR156434
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Direct Submission
Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University
School of Dentistry, Department of Biochemistry: 19-1 Uchimaru,
Morioka, Iwate 020-8505, Japan (E-mail:mnagai@iwate-med.ac.jp,
Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)
Location/Qualifiers
                                                               AR156434
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/protein_id="baa90488.1"
/protein_id="baa90488.1"
/db_xref="GI:6863048"
/translation="modnrISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR
RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQFFAHLTINATDI
PSGSHKVSLSSWYLDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLAT
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EVSNPSLLDPDQDATYFGAFKVRDID"
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/tissue_type="tongue"
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/db_xref="taxon:9606"
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                             ACCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCA---
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Dougall,W.C. and Galibert,L.
Dougall,W.C. and Galibert,L.
Receptor activator of NF. kappa.B
Patent: US 6271349-A 12 07-AUG-2001;
Location/Qualifiers
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GRSMFVALLGLGLGQVVCSVALFFYFRAMDPRIZSEDGTHCIYRILRHENADFQDT
TLESQDTKLIPDSCRIKOAFOGAVOKELOHIVGSOHIRAEKAMVDGSULDLAKRSKL
EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYA
NICFFHHETSGDLATEYLOLWYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRGSGEISIEVSUPSLLDPOQDATYFGAFKVRDID"
239 c 227 g 233 t
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/protein_id="CAC41185.1"
/db_xref="GI:14346965"
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DEFINITION

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Unpublished 2 (bases 1
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HOMO sapiens hRANKL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
                                 Determination of human RANKL isoforms
                                                    Ikeda, T., Kuroyama, H. and Hirokawa, K.
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                     Homo sapiens
                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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SRSMFVALLGLGLGQVVCSVALFFYERAQMDPNRISEDGTHCIYRILRLHENADFQDT
TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIYGSQHIRAEXAMVDGSWLDLAKRSKL
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NICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEPHFYSIN
VGGFFKLMSGEEISIEVSNPSLLDPQDATYFGAFKVRDID"
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/codon_start=1
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/db_xref="GI:21698736"
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/db_xref="taxon:9606"
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Ikeda,T. and Kuroyama,H.
Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                Homo sapiens
                                                                             Unpublished
                                                                                             Determination of human RANKL
                                                                                                           Ikeda,T., Kuroyama,H. and Hirokawa,K.
                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                              Homo sapiens cDNA to mRNA.
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                                                                                                                                                                                                                                                                 Homo sapiens hRANKI 1 mRNA for receptor activator of nuclear factor kappa B ligand 1, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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ligand 2-2"
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Pred. No. 1.3e-27;
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                                                            A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function Nature 390 (6656), 175-179 (1997)
                               9367155
                                                                                                                        Anderson,D.M., Maraskovsky,E., Blilingsley,w.u., L...
Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBose,R.F.,
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2201)
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Homo sapiens receptor activator of nuclear factor kappa B ligand
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Pred. No. 1.3e-27;
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Search completed: December Job time: 2708.23 secs

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Submitted (13-AUG-1997) Molecular Biology,
University St., Seattle, WA 98101, USA
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